

OM protein - protein search, using sw model
Run on: February 7, 2006, 16:07:31 ; Search time 204 Seconds
(without alignments)
1287.983 Million cell updates/sec

Title: US-10-677-669-69
Perfect score: 3135
Sequence: 1 MCSRVLLPLLLLLALGPG.....PLMGFFGQLQSPHLHAKPYI 598
Scoring table: BLOSUM62
Searched: Gapop 10.0 , Gapext 0.5
Total number of hits satisfying chosen parameters: 2443163
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%

Database : A_Geneseq_21.*
Listing first 1500 summaries

1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No. Score Match Length DB ID Description

RESULT 1

ID AAY06484 standard; protein; 598 AA.
DE Human tumour-associated protein PRO357.
PN WO9935170-A2.
PD 15-JUL-1999.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3135; DB 2; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;

RESULT 2

ID AAB01322 standard; protein; 598 AA.
DE Human PRO357 polypeptide.
PN WO200032776-A2.
PD 08-JUN-2000.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3135; DB 3; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;

RESULT 3

ID AAY93691 standard; protein; 598 AA.
DE Amino acid sequence of novel polypeptide PRO357.
PN WO200037640-A2.
PD 29-JUN-2000.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3135; DB 3; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;

RESULT 4

ID AAU83643 standard; protein; 598 AA.
DE Human PRO protein, Seq ID No 104.
PN WO200208288-A2.
PD 31-JAN-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3135; DB 5; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;

RESULT 5

ID ADY31844 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN WO200193983-A1.
PD 13-DEC-2001.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3135; DB 5; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;

RESULT 6

ID ABUS5931 standard; protein; 598 AA.
DE Human secreted/transmembrane protein PRO357.

PN US2002142959-A1.
PD 03-OCT-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;

RESULT 7

ID ABUS0790 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003036635-A1.
PD 20-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;

RESULT 8

ID ABO33756 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003045687-A1.
PD 06-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;

RESULT 9

ID ABUS0241 standard; protein; 598 AA.
DE Human PRO polypeptide #12.
PN US2002132768-A1.
PD 19-SEP-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;

RESULT 10

ID ABUS64927 standard; protein; 598 AA.
DE Human secreted/transmembrane protein PRO357.
PN US2002173463-A1.
PD 21-NOV-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;

RESULT 11

ID ABUS8361 standard; protein; 598 AA.
DE Novel human secreted protein PRO357.
PN US2002150976-A1.
PD 17-OCT-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;

RESULT 12

ID ABUS7247 standard; protein; 598 AA.
DE Human PRO357 protein.
PN US2002142958-A1.
PD 03-OCT-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;

RESULT 13

ID ABUS6312 standard; protein; 598 AA.
DE Human secreted/transmembrane protein, PRO357.
PN US2002132981-A1.
PD 19-SEP-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;

RESULT 14

ID ABUS6352 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2002168715-A1.
PD 14-NOV-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;

RESULT 15

ID ABUS2099 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003088063-A1.

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PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 16
ID ABU11313 standard; protein; 598 AA.
DE Human PRO357 protein sequence.
PN US2002127643-A1.
PD 12-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 17
ID ABU67112 standard; protein; 598 AA.
DE Human PRO polypeptide #12.
PN US2002165143-A1.
PD 07-NOV-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 18
ID ABJ72279 standard; protein; 598 AA.
DE Human PRO357 protein.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 19
ID ABJ72407 standard; protein; 598 AA.
DE Human PRO357 protein.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 20
ID ABO34302 standard; protein; 598 AA.
DE Human secreted/transmembrane polypeptide PRO 357.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 21
ID ABJ72109 standard; protein; 598 AA.
DE Human membrane bound receptor/protein PRO357 amino acid sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 22
ID ADB83594 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 23
ID ADB80700 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003088068-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 24
ID ADB73241 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003096968-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 25
ID ADB78323 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 26
ID ADB84971 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 27
ID ADB78077 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 28
ID ADB87143 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 29
ID ADB84725 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 30
ID ADB83840 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 31
ID ADB72995 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 32
ID ADC25825 standard; protein; 598 AA.
DE Human secreted/transmembrane PRO polypeptide #12.
PN US2002142419-A1.
PD 03-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 33
ID ADC25583 standard; protein; 598 AA.
DE Human secreted/transmembrane PRO polypeptide #12.
PN US2002156004-A1.
PD 24-OCT-2002.
PA (GETH ) GENENTECH INC.
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Query Match 100.0%; Score 3135; DB 7; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 34
 ID ADC25704 standard; protein; 598 AA.
 DE Human secreted/transmembrane PRO polypeptide #12.
 PN US2003077698-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 7; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 35
 ID ADC36833 standard; protein; 598 AA.
 DE Human PRO polypeptide #52.
 PN US2003088065-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 7; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 36
 ID ADC21823 standard; protein; 598 AA.
 DE Human PRO polypeptide #52.
 PN US2003096969-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 7; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 37
 ID ADC49854 standard; protein; 598 AA.
 DE Novel human secreted and transmembrane protein PRO357.
 PN US2003088064-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 7; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 38
 ID ADC49053 standard; protein; 598 AA.
 DE Novel human secreted and transmembrane protein PRO357.
 PN US2003088070-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 7; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 39
 ID ADC49570 standard; protein; 598 AA.
 DE Novel human secreted and transmembrane protein PRO357.
 PN US2003088071-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 7; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 40
 ID ADC47431 standard; protein; 598 AA.
 DE Novel human secreted and transmembrane protein PRO357.
 PN US2003088072-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 7; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 41
 ID ADC47176 standard; protein; 598 AA.
 DE Novel human secreted and transmembrane protein PRO357.
 PN US2003105288-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 7; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 42
 ID ADC78051 standard; protein; 598 AA.
 DE Novel human secreted and transmembrane protein PRO357.
 PN US2003096972-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 7; Length 598;

Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 43
 ID ADD06286 standard; protein; 598 AA.
 DE Novel human secreted and transmembrane protein PRO357.
 PN US2003073816-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 7; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 44
 ID ADC77805 standard; protein; 598 AA.
 DE Novel human secreted and transmembrane protein PRO357.
 PN US2003088066-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 7; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 45
 ID ADD50768 standard; protein; 598 AA.
 DE Novel human secreted and transmembrane protein PRO357.
 PN US2003105291-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 7; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 46
 ID ADD51014 standard; protein; 598 AA.
 DE Novel human secreted and transmembrane protein PRO357.
 PN US2003105290-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 7; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 47
 ID ADD50495 standard; protein; 598 AA.
 DE Human PRO polypeptide #52.
 PN US2003096971-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 7; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 48
 ID ADD50249 standard; protein; 598 AA.
 DE Human PRO polypeptide #52.
 PN US2003096970-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 7; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 49
 ID ADD51260 standard; protein; 598 AA.
 DE Novel human secreted and transmembrane protein PRO357.
 PN US2003105289-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 7; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 50
 ID ADH27489 standard; protein; 598 AA.
 DE Human secreted/transmembrane PRO polypeptide #12.
 PN US2003083479-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 7; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 51
 ID ADC48807 standard; protein; 598 AA.
 DE Novel human secreted and transmembrane protein PRO357.
 PN US2003092888-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 8; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;

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RESULT 52
ID ADE20978 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 53
ID ADE05822 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 54
ID ADD75051 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 55
ID ADD75797 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 56
ID ADD86855 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 57
ID ADE20732 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 58
ID ADE39029 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 59
ID ADE05576 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 60
ID ADE05576 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 61
ID ADE20978 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 62
ID ADD78401 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 63
ID ADE21224 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 64
ID ADD77339 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 65
ID ADE20486 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 66
ID ADD75551 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 67
ID ADD74067 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 68
ID ADD74313 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 69
ID ADD76043 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 70
ID ADD85535 standard; protein; 598 AA.
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DE Novel human secreted and transmembrane protein PRO357.
PN US2003100721-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 71
ID ADE05084 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 72
ID ADD75297 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 73
ID ADD76841 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 74
ID ADD86609 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 75
ID ADD78077 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 76
ID ADE71538 standard; protein; 598 AA.
DE Human secreted/transmembrane PRO polypeptide #12.
PN US2003096742-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 77
ID ADD77585 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 78
ID ADD77831 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 79
ID ADD85289 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.

PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 80
ID ADD73821 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 81
ID ADD74559 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 82
ID ADD77087 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 83
ID ADD85781 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 84
ID ADE05330 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 85
ID ADD74805 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 86
ID ADG05617 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 87
ID ADG27171 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 88
ID ADG11234 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003096967-A1.

PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 8; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 89
 ID ADG12013 standard; protein; 598 AA.
 DE Novel human secreted and transmembrane protein PRO357.
 PN US2003096963-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 8; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 90
 ID ADF94570 standard; protein; 598 AA.
 DE Novel human secreted and transmembrane protein PRO357.
 PN US2003096964-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 8; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 91
 ID ADG6666 standard; protein; 598 AA.
 DE Human PRO polypeptide #52.
 PN US2003096966-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 8; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 92
 ID ADG63481 standard; protein; 598 AA.
 DE Human secreted/transmembrane PRO polypeptide #12.
 PN US2003211570-A1.
 PD 13-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 8; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 93
 ID ADH39010 standard; protein; 598 AA.
 DE Novel human secreted and transmembrane protein PRO357.
 PN US2003096965-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 8; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 94
 ID ADH43210 standard; protein; 598 AA.
 DE Human secreted/transmembrane PRO polypeptide #12.
 PN US2003207401-A1
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 8; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 95
 ID ADG34100 standard; protein; 598 AA.
 DE Novel human secreted and transmembrane protein PRO357.
 PN US2004006206-A1.
 PD 08-JAN-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 8; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 96
 ID ADI33570 standard; protein; 598 AA.
 DE Human PRO polypeptide #52.
 PN US2003096960-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 8; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 97
 ID ADH69664 standard; protein; 598 AA.
 DE Human PRO polypeptide #52.
 PN US2004019183-A1.
 PD 29-JAN-2004.

PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 8; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 98
 ID ADI29825 standard; protein; 598 AA.
 DE Novel human secreted and transmembrane protein PRO357.
 PN US2003096961-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 8; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 99
 ID ADM27222 standard; protein; 598 AA.
 DE Novel human secreted and transmembrane protein PRO357.
 PN US2004044179-A1.
 PD 04-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 8; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 100
 ID ADK6580 standard; protein; 598 AA.
 DE Human PRO polypeptide #52.
 PN US2004044180-A1.
 PD 04-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 8; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 101
 ID ADN00448 standard; protein; 598 AA.
 DE Human secreted/transmembrane PRO polypeptide #12.
 PN US2004091972-A1.
 PD 13-MAY-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 8; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 102
 ID ADU25372 standard; protein; 598 AA.
 DE Human secreted/transmembrane PRO polypeptide #12.
 PN US2004220385-A1.
 PD 04-NOV-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 8; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 103
 ID ADX39535 standard; protein; 598 AA.
 DE Human insulin-like growth factor homolog PRO357 precursor protein.
 PN US2005048613-A1.
 PD 03-MAR-2005.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 9; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 104
 ID ADY73816 standard; protein; 598 AA.
 DE Human PRO357 protein, SEQ ID NO: 69.
 PN US2005059115-A1.
 PD 17-MAR-2005.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 9; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 105
 ID AAV17831 standard; protein; 598 AA.
 DE Human PRO357 protein sequence.
 PN WO9928462-A2.
 PD 10-JUN-1999.
 PA (GETH) GENENTECH INC.
 Query Match 99.7%; Score 3126; DB 2; Length 598;
 Best Local Similarity 99.8%; Pred. No. 1.4e-189;
 RESULT 106
 ID AAB07428 standard; protein; 673 AA.
 DE Amino acid sequence of a leucine-rich surface glycoprotein (LRSG).
 PN WO20042170-A1.
 PD 20-JUL-2000.
 PA (MILL-) MILLENNIUM BIOTHEAPEUTICS INC.

Query Match 98.4%; Score 3083.5; DB 3; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 107
ID AAB87533 standard; protein; 673 AA.
DE Human PRO1282.
PN WO200116318-A2.
PD 08-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 4; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 108
ID AAB6166 standard; protein; 673 AA.
DE Human PRO1282 (UNQ652) protein sequence SEQ ID NO:52.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 4; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 109
ID AAU75266 standard; protein; 673 AA.
DE Human Slit-like protein #1.
PN WO200212346-A2.
PD 14-FEB-2002.
PA (PHAA) PHARMACIA CORP.
Query Match 98.4%; Score 3083.5; DB 5; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 110
ID ABG95858 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2002119130-A1.
PD 29-AUG-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 5; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 111
ID ABG78042 standard; protein; 673 AA.
DE Human leucine-rich surface glycoprotein (LRSG-1).
PN US2002072089-A1.
PD 13-JUN-2002.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (MACB/) MACBETH K J.
PA (BUSF/) BUSFIELD S J.
PA (PANY/) PAN Y.
PA (WHIT/) WHITE D.
PA (KHOD/) KHODADOUST M M.
PA (GUWW/) GU W.
Query Match 98.4%; Score 3083.5; DB 5; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 112
ID ABUS7981 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003027163-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 113
ID ABUS9059 standard; protein; 673 AA.
DE Novel human secreted or transmembrane protein PRO1282.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 114
ID ABUS2571 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003032023-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 115
ID ABUS9206 standard; protein; 673 AA.
DE Human secreted/transmembrane protein, #19.

DE Human secreted/transmembrane protein, #19.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 116
ID ABUI3872 standard; protein; 673 AA.
DE Human PRO1282 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 117
ID ABU72457 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 118
ID ABUS9083 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 119
ID ABO33942 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 120
ID ABU71959 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 121
ID ABU71513 standard; protein; 673 AA.
DE Human secreted polypeptide PRO1282.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 122
ID ABU72294 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 123
ID ABUS9067 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 124
ID ABUS9206 standard; protein; 673 AA.
DE Human secreted/transmembrane protein, #19.

PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 125
ID ABO25903 standard; protein; 673 AA.
DE Human PRO1282 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 126
ID ABO27288 standard; protein; 673 AA.
DE Human secreted/transmembrane polypeptide PRO1282.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 127
ID ABO2483 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 128
ID ABO81153 standard; protein; 673 AA.
DE Human secreted polypeptide PRO1282.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 129
ID ABO33268 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 130
ID ABUS8912 standard; protein; 673 AA.
DE Human secreted/transmembrane protein, #19.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 131
ID ABUS2290 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003022187-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 132
ID ABUS9355 standard; protein; 673 AA.
DE Novel human secreted or transmembrane protein PRO1282.
PN US2003027985-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 133
ID ABO38270 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 134
ID ABUS9275 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 135
ID ABUS2482 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 136
ID ABUS2121 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003017476-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 137
ID ABUS6446 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 138
ID ABUI0827 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 139
ID ABUS1579 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 140
ID ABUS2116 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 141
ID ABUS8518 standard; protein; 673 AA.
DE Human secreted and transmembrane polypeptide PRO1282.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 142
ID ABO34032 standard; protein; 673 AA.
DE Human PRO1282 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 143
ID ADBI7073 standard; protein; 673 AA.

DE Human transmembrane PRO polypeptide (SeqID 16).
PN US2003050462-A1.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 144
ID ADA37563 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 145
ID ADA21249 standard; protein; 673 AA.
DE Human secreted/transmembrane polypeptide PRO1282.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 146
ID ABO44246 standard; protein; 673 AA.
DE Human secreted/transmembrane polypeptide PRO 1282.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 147
ID ADA10036 standard; protein; 673 AA.
DE Human secreted/transmembrane protein, PRO1282.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 148
ID ADA19878 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 149
ID ADB17261 standard; protein; 673 AA.
DE Human transmembrane PRO polypeptide (SeqID 16).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 150
ID ADA17580 standard; protein; 673 AA.
DE Human PRO1282 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 151
ID ADA27688 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003054359-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 152
ID ADA20050 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;

Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 153
ID ABO34174 standard; protein; 673 AA.
DE Human secreted/transmembrane polypeptide PRO 1282.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 154
ID ADA94268 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003059832-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 155
ID ADA38493 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003059780-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 156
ID ADA92614 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003060407-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 157
ID ADA00347 standard; protein; 673 AA.
DE Human secreted/transmembrane polypeptide PRO 1282.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 158
ID ABO53118 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003044806-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 159
ID ADA22175 standard; protein; 673 AA.
DE Human secreted/transmembrane polypeptide PRO1282.
PN US2003040473-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 160
ID ABO22488 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003017982-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 161
ID ADA06341 standard; protein; 673 AA.
DE Human secreted/transmembrane PRO polypeptide #13.
PN US2003049638-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 162
ID ADA39034 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003059782-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;

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RESULT 163
ID ADB95589 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 7; Length 673;
88.7%; Pred. No. 8.1e-187;
RESULT 164
ID ADB96060 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 7; Length 673;
88.7%; Pred. No. 8.1e-187;
RESULT 165
ID ADB68268 standard; protein; 673 AA.
DE Human PRO1282 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 7; Length 673;
88.7%; Pred. No. 8.1e-187;
RESULT 166
ID ADB68075 standard; protein; 673 AA.
DE Human PRO1282 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 7; Length 673;
88.7%; Pred. No. 8.1e-187;
RESULT 167
ID ADB90892 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 7; Length 673;
88.7%; Pred. No. 8.1e-187;
RESULT 168
ID ADC57532 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003027754-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 7; Length 673;
88.7%; Pred. No. 8.1e-187;
RESULT 169
ID ADC54896 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003045463-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 7; Length 673;
88.7%; Pred. No. 8.1e-187;
RESULT 170
ID ADC11763 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003049681-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 7; Length 673;
88.7%; Pred. No. 8.1e-187;
RESULT 171
ID ADC06972 standard; protein; 673 AA.
DE Human PRO1282 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 7; Length 673;
88.7%; Pred. No. 8.1e-187;
RESULT 172
ID ADC56185 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003064375-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 7; Length 673;
88.7%; Pred. No. 8.1e-187;
RESULT 173
ID ADC17151 standard; protein; 673 AA.
DE Mammalian PRO polypeptide (seqID 16).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 7; Length 673;
88.7%; Pred. No. 8.1e-187;
RESULT 174
ID ADC07240 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003068447-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 7; Length 673;
88.7%; Pred. No. 8.1e-187;
RESULT 175
ID ADC11230 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003069403-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 7; Length 673;
88.7%; Pred. No. 8.1e-187;
RESULT 176
ID ADC14849 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 7; Length 673;
88.7%; Pred. No. 8.1e-187;
RESULT 177
ID ADC52344 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 7; Length 673;
88.7%; Pred. No. 8.1e-187;
RESULT 178
ID ADC14352 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003082546-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 7; Length 673;
88.7%; Pred. No. 8.1e-187;
RESULT 179
ID ADD07884 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003068623-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 7; Length 673;
88.7%; Pred. No. 8.1e-187;
RESULT 180
ID ADC81709 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003083461-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 7; Length 673;
88.7%; Pred. No. 8.1e-187;
RESULT 181
ID ADD07351 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 7; Length 673;
88.7%; Pred. No. 8.1e-187;
RESULT 182
ID ADC82242 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003059833-A1.
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PD 27-MAR-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 183
ID ADD08422 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 184
ID ADD06671 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 185
ID ADC82918 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 186
ID ADD55025 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 187
ID ADD36020 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 188
ID ADD55983 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 189
ID ADD54421 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 190
ID ADE26575 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 191
ID ADE26042 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 192
ID ADF66979 standard; protein; 673 AA.
DE Human PRO1282 amino acid sequence SEQ ID NO:52.
PN US2002198148-A1.

PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 193
ID ADG01021 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 194
ID ADG08574 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 195
ID ADF95195 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 196
ID ADH24048 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 197
ID ADH34074 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 198
ID ADH29907 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 199
ID ADH23878 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 200
ID ADG85282 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 201
ID ADH24558 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180907-A1.
PD 25-SEP-2003.

Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 220
ID ADI25534 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 221
ID ADH97708 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 222
ID ADI35233 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 223
ID ADI03556 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 224
ID ADI11913 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 225
ID ADH89987 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 226
ID ADH99725 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 227
ID ADH98388 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 228
ID ADI11063 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 229
ID ADI11573 standard; protein; 673 AA.

DE Human PRO polypeptide #8.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 230
ID ADH98218 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 231
ID ADH98558 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 232
ID ADH98048 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 233
ID ADI05036 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 234
ID ADI03386 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 235
ID ADI04781 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 236
ID ADH78235 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181688-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 237
ID ADI19579 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 238
ID ADH90327 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.

PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 239
ID ADI03046 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 240
ID ADH77895 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 241
ID ADH97878 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 242
ID ADI01263 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 243
ID ADI01958 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 244
ID ADI03216 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 245
ID ADI11403 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 246
ID ADI02305 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 247
ID ADI11743 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181685-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 248
ID ADI05380 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 249
ID ADH79452 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 250
ID ADI19409 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 251
ID ADI05210 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 252
ID ADH79622 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 253
ID ADI01448 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 254
ID ADI01618 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 255
ID ADI01788 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 256
ID ADH79792 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003191289-A1.
PD 09-OCT-2003.

PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 257
ID ADI04610 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 258
ID ADI02746 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 259
ID ADH78065 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 260
ID ADI25704 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 261
ID ADI25874 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 262
ID ADK65386 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 263
ID ADH98728 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 264
ID ADH79969 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 265
ID ADL93700 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.

Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 266
ID ADC52154 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 267
ID ADF35178 standard; protein; 673 AA.
DE Human PRO1282 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 268
ID ADG11428 standard; protein; 673 AA.
DE Human PRO1282 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 269
ID ADH06586 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 270
ID ADH06416 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 271
ID ADG68837 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 272
ID ADH27727 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 273
ID ADH25068 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 274
ID ADH33700 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 275
ID ADL93700 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.

RESULT 275
ID ADH02343 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 276
ID ADH07950 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 277
ID ADG69347 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 278
ID ADH39168 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 279
ID ADG81908 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 280
ID ADH19298 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 281
ID ADG85452 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 282
ID ADH06246 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 283
ID ADH30076 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 284
ID ADH20791 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 285
ID ADG8517 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 286
ID ADH07780 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 287
ID ADG85792 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 288
ID ADH39338 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 289
ID ADH33530 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 290
ID ADH33870 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 291
ID ADH01080 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 292
ID ADG69687 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 293
ID ADH20791 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 293

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DE Human secreted/transmembrane protein PRO1282.
PD US2003224358-A1.
  Query Match      98.4%; Score 3083.5; DB 8; Length 673;
  Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 294
ID ADH02173 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PD US2003180841-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      98.4%; Score 3083.5; DB 8; Length 673;
  Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 295
ID ADG69177 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PD US2003180847-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      98.4%; Score 3083.5; DB 8; Length 673;
  Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 296
ID ADG85962 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PD US2003180862-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      98.4%; Score 3083.5; DB 8; Length 673;
  Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 297
ID ADH24898 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PD US2003180909-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      98.4%; Score 3083.5; DB 8; Length 673;
  Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 298
ID ADH39515 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PD US2003180915-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      98.4%; Score 3083.5; DB 8; Length 673;
  Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 299
ID ADH19831 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PD US2003219856-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match      98.4%; Score 3083.5; DB 8; Length 673;
  Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 300
ID ADH02513 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PD US2003180840-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      98.4%; Score 3083.5; DB 8; Length 673;
  Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 301
ID ADG69007 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PD US2003180849-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      98.4%; Score 3083.5; DB 8; Length 673;
  Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 302
ID ADH07610 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PD US2003180850-A1.
  Query Match      98.4%; Score 3083.5; DB 8; Length 673;
  Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 303
ID ADG86132 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PD US2003180863-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      98.4%; Score 3083.5; DB 8; Length 673;
  Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 304
ID ADH24728 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PD US2003180908-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      98.4%; Score 3083.5; DB 8; Length 673;
  Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 305
ID ADH25776 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PD US2003180911-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      98.4%; Score 3083.5; DB 8; Length 673;
  Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 306
ID ADH38342 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PD US2003180922-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      98.4%; Score 3083.5; DB 8; Length 673;
  Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 307
ID ADH57181 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PD US2003181642-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      98.4%; Score 3083.5; DB 8; Length 673;
  Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 308
ID ADH52169 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PD US2003180921-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      98.4%; Score 3083.5; DB 8; Length 673;
  Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 309
ID ADH49535 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PD US2003180857-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      98.4%; Score 3083.5; DB 8; Length 673;
  Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 310
ID ADH90497 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PD US2003181700-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match      98.4%; Score 3083.5; DB 8; Length 673;
  Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 311
ID ADI11233 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PD US2003181683-A1.
PD 25-SEP-2003.
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PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 312
ID ADH98898 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 313
ID ADI02128 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 314
ID ADH98667 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 315
ID ADJ98542 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 316
ID ADJ98712 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 317
ID ADH78871 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 318
ID ADJ99105 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 319
ID ADJ99275 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 320
ID ADJ98893 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 321
ID ADH79041 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 322
ID ADK00901 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 323
ID ADK1422 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 324
ID ADM80871 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 325
ID ADR45587 standard; protein; 673 AA.
DE Human leucine-rich surface glycoprotein, LRSG-1, protein #1.
PN US2004176296-A1.
PD 09-SEP-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 326
ID ADY77711 standard; protein; 673 AA.
DE Neoplastic disease detection protein PRO1282.
PN US2005059102-A1.
PD 17-MAR-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match 98.4%; Score 3083.5; DB 9; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 327
ID AEA38367 standard; protein; 673 AA.
DE Human secreted/transmembrane protein, #81.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 9; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 328
ID AAB84689 standard; protein; 673 AA.
DE Amino acid sequence of human slit polypeptide Zslit3.
PN WO200146418-A1.
PD 28-JUN-2001.
PA (ZYMO ) ZYMOGENETICS INC.
Query Match 98.2%; Score 3078.5; DB 4; Length 673;
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Best Local Similarity 88.6%; Pred. No. 1.7e-186;
 RESULT 329
 ID ADF69108 standard; protein; 673 AA.
 DE Human MP53 protein sequence SEQ ID NO:78.
 PN WO2003083047-A2.
 PD 09-OCT-2003.
 PA (EXEL-) EXELIXIS INC.
 Query Match 98.2%; Score 3078.5; DB 7; Length 673;
 Best Local Similarity 88.6%; Pred. No. 1.7e-186;
 RESULT 330
 ID ABO59449 standard; protein; 676 AA.
 DE Human genome derived single exon protein #5683.
 PN US2003194704-A1.
 PD 16-OCT-2003.
 PA (PENN/) PENN S G.
 PA (RANK/) RANK D R.
 PA (HANZ/) HANZEL D K.
 Query Match 98.2%; Score 3078.5; DB 8; Length 676;
 Best Local Similarity 88.6%; Pred. No. 1.7e-186;
 RESULT 331
 ID ADA57213 standard; protein; 672 AA.
 DE Human secreted protein #496.
 PN WO2002102994-A2.
 PD 27-DEC-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 93.6%; Score 2935; DB 6; Length 672;
 Best Local Similarity 85.2%; Pred. No. 2.1e-177;
 RESULT 332
 ID ADA41092 standard; protein; 672 AA.
 DE Human secreted protein.
 PN WO2002102993-A2.
 PD 27-DEC-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 93.6%; Score 2935; DB 6; Length 672;
 Best Local Similarity 85.2%; Pred. No. 2.1e-177;
 RESULT 333
 ID ABR47923 standard; protein; 672 AA.
 DE Human secreted protein, SEQ ID 814.
 PN WO200295010-A2.
 PD 28-NOV-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 93.8%; Score 2935; DB 6; Length 672;
 Best Local Similarity 85.2%; Pred. No. 2.1e-177;
 RESULT 334
 ID AAB38323 standard; protein; 673 AA.
 DE Human secreted protein encoded by gene 3 clone HSYAV50.
 PN WO200061623-A1.
 PD 19-OCT-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 93.6%; Score 2935; DB 3; Length 673;
 Best Local Similarity 85.2%; Pred. No. 2.1e-177;
 RESULT 335
 ID AAB38400 standard; peptide; 723 AA.
 DE Fragment of human secreted protein encoded by gene 3 clone HSYAV50.
 PN WO200061623-A1.
 PD 19-OCT-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 93.6%; Score 2935; DB 3; Length 723;
 Best Local Similarity 85.2%; Pred. No. 2.2e-177;
 RESULT 336
 ID AAU75267 standard; protein; 630 AA.
 DE Human Slit-like protein #2.
 PN WO200212346-A2.
 PD 14-FEB-2002.
 PA (PHAR-) PHARMACIA CORP.
 Query Match 90.8%; Score 2845.5; DB 5; Length 630;
 Best Local Similarity 85.2%; Pred. No. 8.9e-172;
 RESULT 337
 ID AAY66643 standard; protein; 611 AA.
 DE Membrane-bound protein PRO1282.
 PN WO963088-A2.
 PD 09-DEC-1999.
 PA (GETH-) GENENTECH INC.
 Query Match 15.0%; Score 471; DB 7; Length 117;
 Best Local Similarity 79.5%; Pred. No. 2.3e-163;
 RESULT 338
 ID ABG78046 standard; protein; 673 AA.
 DE Mouse leucine-rich surface glycoprotein (LRSG-1).
 PN US2002072089-A1.
 PD 13-JUN-2002.
 PA (HOLT/) HOLTZMAN D A.
 PA (MCCA/) MCCARTHY S A.
 PA (MACE/) MACBETH K J.
 PA (BUSF/) BUSFIELD S J.
 PA (PANI/) PAN Y.
 PA (WHIT/) WHITE D.
 PA (KHOD/) KHODADOUST M M.
 PA (GUWW/) GU W.
 Query Match 79.4%; Score 2490; DB 5; Length 673;
 Best Local Similarity 73.5%; Pred. No. 3.2e-149;
 RESULT 339
 ID ADR45596 standard; protein; 673 AA.
 DE Human leucine-rich surface glycoprotein, LRSG-1, protein #2.
 PN US2004176296-A1.
 PD 09-SEP-2004.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 79.4%; Score 2490; DB 8; Length 673;
 Best Local Similarity 73.5%; Pred. No. 3.2e-149;
 RESULT 340
 ID ADA00753 standard; protein; 673 AA.
 DE Murine stromal cell derived haematopoietin factor-5 SEQ ID NO:10.
 PN WO2003018805-A1.
 PD 06-MAR-2003.
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 PA (NINA-) JAPAN NAT CANCER CENT.
 Query Match 79.2%; Score 2484; DB 6; Length 673;
 Best Local Similarity 73.4%; Pred. No. 7.7e-149;
 RESULT 341
 ID AAB07431 standard; protein; 493 AA.
 DE A leucine-rich surface glycoprotein (LRSG).
 PN WO200042170-A1.
 PD 20-JUL-2000.
 PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
 Query Match 53.3%; Score 1672; DB 3; Length 493;
 Best Local Similarity 53.3%; Pred. No. 1.5e-97;
 RESULT 342
 ID ABB72324 standard; protein; 281 AA.
 DE Rat protein isolated from skin cells SEQ ID NO: 648.
 PN WO200190357-A1.
 PD 29-NOV-2001.
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 Query Match 37.6%; Score 1178.5; DB 5; Length 281;
 Best Local Similarity 80.7%; Pred. No. 1.4e-66;
 RESULT 343
 ID AAO30403 standard; protein; 311 AA.
 DE Human secreted protein (SECP)-6.
 PN WO2003046196-A1.
 PD 05-JUN-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 31.8%; Score 997.5; DB 7; Length 311;
 Best Local Similarity 68.7%; Pred. No. 4.6e-55;
 RESULT 344
 ID ABR58506 standard; protein; 307 AA.
 DE Human secreted protein Incyte ID No: 7500228CD1 SEQ ID NO: 18.
 PN WO2003029437-A2.
 PD 10-APR-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 31.3%; Score 980.5; DB 6; Length 307;
 Best Local Similarity 67.9%; Pred. No. 5.5e-54;
 RESULT 345
 ID AAO30821 standard; protein; 117 AA.
 DE Human cell adhesion and extracellular matrix protein (CAECM)-11.
 PN WO2003047526-A2.
 PD 12-JUN-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 15.0%; Score 471; DB 7; Length 117;

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Best Local Similarity 98.9%; Pred. No. 3.4e-22;
RESULT 346
ID AAE23980 standard; protein; 635 AA.
DE Human LP220 secreted protein.
PN WO200226801-A2.
PD 04-APR-2002.
PA (ELJL ) LILLY & CO ELI.
Query Match 11.5%; Score 360.5; DB 5; Length 635;
Best Local Similarity 27.1%; Pred. No. 2.4e-14;
RESULT 347
ID ABP70142 standard; protein; 647 AA.
DE Human NOV44a.
PN WO200272771-A2.
PD 19-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 11.5%; Score 360.5; DB 5; Length 647;
Best Local Similarity 27.1%; Pred. No. 2.5e-14;
RESULT 348
ID AAO26256 standard; protein; 635 AA.
DE MDDT related human protein SEQ ID No 34.
PN WO200296951-A1.
PD 05-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 11.5%; Score 359.5; DB 6; Length 635;
Best Local Similarity 27.6%; Pred. No. 2.8e-14;
RESULT 349
ID ADZ09859 standard; protein; 635 AA.
DE Human breast cancer marker MGC3103 protein.
PN EP1522594-A2.
PD 13-APR-2005.
PA (FARB ) BAYER HEALTHCARE AG.
Query Match 11.5%; Score 359.5; DB 9; Length 635;
Best Local Similarity 27.6%; Pred. No. 2.8e-14;
RESULT 350
ID ABP70144 standard; protein; 778 AA.
DE Human NOV44c.
PN WO200272771-A2.
PD 19-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 11.4%; Score 357.5; DB 5; Length 778;
Best Local Similarity 26.7%; Pred. No. 4.8e-14;
RESULT 351
ID ADM90979 standard; protein; 545 AA.
DE Human pharmaceutically useful protein SeqID 372.
PN WO2004020595-A2.
PD 11-MAR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
PA (RIKE-) RIKEN INST PHYSICAL & CHEM RES.
PA (DNAF-) DNAFORM KK.
Query Match 11.2%; Score 350.5; DB 8; Length 545;
Best Local Similarity 27.9%; Pred. No. 8.7e-14;
RESULT 352
ID ABP70143 standard; protein; 566 AA.
DE Human NOV44b.
PN WO200272771-A2.
PD 19-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 10.8%; Score 339; DB 5; Length 566;
Best Local Similarity 26.9%; Pred. No. 4.9e-13;
RESULT 353
ID AAE17484 standard; protein; 551 AA.
DE Human leucine-rich repeat-8 (ZLR8) protein #2.
PN WO200202604-A2.
PD 10-JAN-2002.
PA (ZYMO ) ZYMOGENETICS INC.
Query Match 10.8%; Score 338; DB 5; Length 551;
Best Local Similarity 27.4%; Pred. No. 5.5e-13;
RESULT 354
ID ADI21104 standard; protein; 618 AA.
DE Novel human prodein #79.
PN WO2003025148-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.

Query Match 10.7%; Score 337; DB 7; Length 618;
Best Local Similarity 27.2%; Pred. No. 7.2e-13;
RESULT 355
ID ADA23287 standard; protein; 653 AA.
DE Human SECX polypeptide, SEC5 #1.
PN US2003054514-A1.
PD 20-MAR-2003.
PA (SHIM/) SHIMKETS R A.
PA (LARO/) LAROCHELLE W J.
Query Match 10.7%; Score 337; DB 6; Length 653;
Best Local Similarity 23.6%; Pred. No. 7.7e-13;
RESULT 356
ID AAB23033 standard; protein; 694 AA.
DE Human SLIT protein-like splice variant, SECX 3352358-1.
PN WO200053742-A2.
PD 14-SEP-2000.
PA (CURA-) CURAGEN CORP.
Query Match 10.7%; Score 337; DB 3; Length 694;
Best Local Similarity 23.6%; Pred. No. 8.3e-13;
RESULT 357
ID AAB23034 standard; protein; 590 AA.
DE Human SLIT protein-like splice variant, SECX 3352358-2.
PN WO200053742-A2.
PD 14-SEP-2000.
PA (CURA-) CURAGEN CORP.
Query Match 10.6%; Score 333; DB 3; Length 590;
Best Local Similarity 25.8%; Pred. No. 1.2e-12;
RESULT 358
ID ADA23289 standard; protein; 590 AA.
DE Human SECX polypeptide, SEC6.
PN US2003054514-A1.
PD 20-MAR-2003.
PA (SHIM/) SHIMKETS R A.
PA (LARO/) LAROCHELLE W J.
Query Match 10.6%; Score 333; DB 6; Length 590;
Best Local Similarity 25.8%; Pred. No. 1.2e-12;
RESULT 359
ID ABG04827 standard; protein; 526 AA.
DE Novel human diagnostic protein #4818.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.6%; Score 332; DB 4; Length 526;
Best Local Similarity 26.9%; Pred. No. 1.2e-12;
RESULT 360
ID AAY28806 standard; protein; 653 AA.
DE cc359.4 secreted protein.
PN WO9950405-A1.
PD 07-OCT-1999.
PA (GENY ) GENETICS INST INC.
Query Match 10.5%; Score 330; DB 2; Length 653;
Best Local Similarity 24.2%; Pred. No. 2.1e-12;
RESULT 361
ID AAY66694 standard; protein; 653 AA.
DE Membrane-bound protein PRO1111.
PN WO9963088-A2.
PD 09-DEC-1999.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 3; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 362
ID AAB24073 standard; protein; 653 AA.
DE Human PRO1111 protein sequence SEQ ID NO.46.
PN WO200053755-A2.
PD 14-SEP-2000.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 3; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 363
ID AAU12390 standard; protein; 653 AA.
DE Human PRO1111 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
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PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 4; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 364
ID AAE09438 standard; protein; 653 AA.
DE Human ebgPRO331a protein.
PN WO200160850-A1.
PD 23-AUG-2001.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 10.5%; Score 330; DB 4; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 365
ID AAB65217 standard; protein; 653 AA.
DE Human PRO1111 (UNQ554) protein sequence SEQ ID NO:229.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 4; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 366
ID ABUS8032 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 367
ID ABUS9110 standard; protein; 653 AA.
DE Novel human secreted or transmembrane protein PRO1111.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 368
ID ABUS2622 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 369
ID ABO17834 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 370
ID ABUS60541 standard; protein; 653 AA.
DE Human secreted/transmembrane protein, #93.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 371
ID ABUS1923 standard; protein; 653 AA.
DE Human PRO1111 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 372
ID ABUS1088 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 373
ID ABUS2508 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 374
ID ABUS66788 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 375
ID AAO23105 standard; protein; 653 AA.
DE NAG14 'human modifier of p53 pathway' protein.
PN WO2003035833-A2.
PD 01-MAY-2003.
PA (EXEL-) EXELIXIS INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 376
ID ABUS9869 standard; protein; 653 AA.
DE Novel secreted and transmembrane protein PRO1111.
PN US2003017583-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 377
ID ABUS9257 standard; protein; 653 AA.
DE Human secreted/transmembrane protein, #93.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 378
ID ABO25954 standard; protein; 653 AA.
DE Human PRO1111 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 379
ID ABO25059 standard; protein; 653 AA.
DE Human secreted/transmembrane protein (PRO) #219.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 380
ID ABUS8963 standard; protein; 653 AA.
DE Human secreted/transmembrane protein, #93.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 381
ID ABUS2341 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 382
ID ABUS9406 standard; protein; 653 AA.

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DE Novel human secreted or transmembrane protein PRO1344.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 383
ID ABU67064 standard; protein; 653 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 438.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 384
ID ABU92172 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003017476-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 385
ID ABU10878 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 386
ID ABU81630 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 387
ID ABU88569 standard; protein; 653 AA.
DE Human secreted and transmembrane polypeptide PRO1111.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 388
ID ABO34083 standard; protein; 653 AA.
DE Human PRO1111 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 389
ID ADA45957 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 390
ID ADA76388 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 391
ID ADA19038 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 392
ID ADA61661 standard; protein; 653 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 393
ID ADB19446 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 394
ID ADB27987 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 395
ID ADA86466 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 396
ID ADB16030 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 397
ID ADA37740 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 398
ID ADA47816 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 399
ID ADA21426 standard; protein; 653 AA.
DE Human secreted/transmembrane polypeptide PRO1111.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 400
ID ADA10213 standard; protein; 653 AA.
DE Human secreted/transmembrane protein, PRO1111.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 401
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ID ADA67611 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 402
ID ADB30618 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 403
ID ADA85914 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 404
ID ADA17757 standard; protein; 653 AA.
DE Human PRO1111 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 405
ID ADA97126 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 406
ID ADA79430 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 407
ID ADA87569 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 408
ID ADB16771 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 409
ID ADA27865 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003054359-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 410
ID ADA91863 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082694-A1.

PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 411
ID ADB14926 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 412
ID ADB18887 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 413
ID ADA94102 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 414
ID ADB19998 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 415
ID ADB13310 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 416
ID ABO43367 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 417
ID ADA94445 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003059832-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 418
ID ADA74564 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 419
ID ADB24797 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 420
ID ADA82321 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 421
ID ADA75284 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 422
ID ADA85362 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 423
ID ADA84810 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 424
ID ADB30066 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 425
ID ADA80594 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 426
ID ADA75836 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 427
ID ADA38670 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 428
ID ADA47061 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;

RESULT 429
ID ADB25357 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 430
ID ADA93533 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 431
ID ADB26883 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 432
ID ADB31170 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 433
ID ADA92791 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 434
ID ADA61098 standard; protein; 653 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 435
ID ADB24245 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 436
ID ADA96574 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 437
ID ADA81146 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 438
ID ADA96022 standard; protein; 653 AA.

DE Human PRO polypeptide #219.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 439
ID ADB26331 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 440
ID ADB21816 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 441
ID ADA77595 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 442
ID ADB18335 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003077110-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 443
ID ADA87018 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 444
ID ADA88121 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 445
ID ADA46509 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 446
ID ADB28539 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 447
ID ADB29091 standard; protein; 653 AA.
DE Human PRO polypeptide #219.

PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 448
ID ABO53169 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003044806-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 449
ID ADA77043 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 450
ID ADA22352 standard; protein; 653 AA.
DE Human secreted/transmembrane polypeptide PRO1111.
PN US2003040473-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 451
ID ADA88673 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 452
ID ADA937678 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 453
ID ADB27435 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003022339-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 454
ID ADB22368 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 455
ID ABO22539 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003017982-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 456
ID ADA06518 standard; protein; 653 AA.
DE Human secreted/transmembrane PRO polypeptide #64.
PN US2003049638-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 457
ID ADA39211 standard; protein; 653 AA.

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DE Human secreted/transmembrane protein PRO1111.
PN US2003059782-A1.
PD 27-MAR-2003.
  Query Match      10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 458
ID ADA67059 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 459
ID ADB22920 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003077111-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 460
ID ADB23693 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
PN US2003077112-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 461
ID ADA92415 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 462
ID ADB15478 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 463
ID ADB38730 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 464
ID ADB96237 standard; protein; 653 AA.
DE Human PRO polypeptide #84.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 465
ID ADB38178 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 466
ID ADB66650 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 467
ID ADB89730 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 468
ID ADB90462 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 469
ID ADB39563 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 470
ID ADB47186 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 471
ID ADB86793 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 472
ID ADB77398 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 473
ID ADB34555 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
PN US200307717-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 474
ID ADB35659 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
PN US200307719-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 475
ID ADB34003 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
PN US200307716-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
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Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 476
ID ADB35107 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 477
ID ADB36211 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 478
ID ADB46606 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 479
ID ADC57709 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 480
ID ADC55073 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 481
ID ADC11940 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 482
ID ADC56362 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 483
ID ADC07417 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 484
ID ADC11407 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 485
ID ADC50479 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003092106-A1.
PD 15-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 486
ID ADC72026 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 487
ID ADC60005 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 488
ID ADC53012 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein Seq ID438.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 489
ID ADC57366 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein Seq ID438.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 490
ID ADC60557 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 491
ID ADC51032 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 492
ID ADC65559 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 493
ID ADC54657 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein Seq ID438.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 494
ID ADC53618 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein Seq ID438.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.

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Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 495
ID ADCS59141 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein Seq ID438.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 496
ID ADCS6019 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein Seq ID438.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 497
ID ADCS8589 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein Seq ID438.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 498
ID ADC14529 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 499
ID ADD08061 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 500
ID ADD03263 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 501
ID ADC90255 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 502
ID ADC81886 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 503
ID ADC69674 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 504
ID ADC48563 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087358-A1.
PD 08-MAY-2003.
DE Human PRO polypeptide #219.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 505
ID ADD10092 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 506
ID ADD07528 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 507
ID ADD04667 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 508
ID ADC82419 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 509
ID ADC80623 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 510
ID ADD11130 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 511
ID ADC48011 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 512
ID ADD08599 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 513
ID ADC80071 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087358-A1.
PD 08-MAY-2003.
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PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 514
ID ADD06848 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 515
ID ADD09540 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 516
ID ADC83095 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 517
ID ADD41253 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 518
ID ADD52392 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 519
ID ADD53132 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 520
ID ADD53684 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 521
ID ADD55202 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 522
ID ADD56160 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 523
ID ADE32379 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 524
ID ADD02639 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 525
ID ADD02073 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 526
ID ADD54255 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 527
ID ADD54598 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 528
ID ADD52572 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 529
ID ADD91468 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 530
ID ADE04082 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 531
ID ADE26752 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 532
ID ADE32379 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
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PN	US2003194765-A1.
PD	16-OCT-2003.
PA	(GETH) GENENTECH INC.
Query Match	10.5%; Score 330; DB 7; Length 653;
Best Local Similarity	24.3%; Pred. No. 2.1e-12;
RESULT 533	
ID	ADE22311 standard; protein; 653 AA.
DE	Human PRO polypeptide #219.
PN	US2003199056-A1.
PD	23-OCT-2003.
PA	(GETH) GENENTECH INC.
Query Match	10.5%; Score 330; DB 7; Length 653;
Best Local Similarity	24.3%; Pred. No. 2.1e-12;
RESULT 534	
ID	ADD79535 standard; protein; 653 AA.
DE	Human PRO polypeptide #219.
PN	US2003203428-A1.
PD	30-OCT-2003.
PA	(GETH) GENENTECH INC.
Query Match	10.5%; Score 330; DB 7; Length 653;
Best Local Similarity	24.3%; Pred. No. 2.1e-12;
RESULT 535	
ID	ADE42071 standard; protein; 653 AA.
DE	Human PRO polypeptide #219.
PN	US2003194772-A1.
PD	16-OCT-2003.
PA	(GETH) GENENTECH INC.
Query Match	10.5%; Score 330; DB 7; Length 653;
Best Local Similarity	24.3%; Pred. No. 2.1e-12;
RESULT 536	
ID	ADE17888 standard; protein; 653 AA.
DE	Human PRO polypeptide #219.
PN	US2003199023-A1.
PD	23-OCT-2003.
PA	(GETH) GENENTECH INC.
Query Match	10.5%; Score 330; DB 7; Length 653;
Best Local Similarity	24.3%; Pred. No. 2.1e-12;
RESULT 537	
ID	ADD92020 standard; protein; 653 AA.
DE	Human PRO polypeptide #219.
PN	US2003199053-A1.
PD	23-OCT-2003.
PA	(GETH) GENENTECH INC.
Query Match	10.5%; Score 330; DB 7; Length 653;
Best Local Similarity	24.3%; Pred. No. 2.1e-12;
RESULT 538	
ID	ADE33483 standard; protein; 653 AA.
DE	Novel human secreted and transmembrane protein PROI111.
PN	US2003194767-A1.
PD	16-OCT-2003.
PA	(GETH) GENENTECH INC.
Query Match	10.5%; Score 330; DB 7; Length 653;
Best Local Similarity	24.3%; Pred. No. 2.1e-12;
RESULT 539	
ID	ADE34035 standard; protein; 653 AA.
DE	Novel human secreted and transmembrane protein PROI111.
PN	US2003194791-A1.
PD	16-OCT-2003.
PA	(GETH) GENENTECH INC.
Query Match	10.5%; Score 330; DB 7; Length 653;
Best Local Similarity	24.3%; Pred. No. 2.1e-12;
RESULT 540	
ID	AD80087 standard; protein; 653 AA.
DE	Human PRO polypeptide #219.
PN	US2003207417-A1.
PD	06-NOV-2003.
PA	(GETH) GENENTECH INC.
Query Match	10.5%; Score 330; DB 7; Length 653;
Best Local Similarity	24.3%; Pred. No. 2.1e-12;
RESULT 541	
ID	ADD93124 standard; protein; 653 AA.
DE	Human PRO polypeptide #219.
PN	US2003194768-A1.
PD	23-OCT-2003.
PA	(GETH) GENENTECH INC.
Query Match	10.5%; Score 330; DB 7; Length 653;
Best Local Similarity	24.3%; Pred. No. 2.1e-12;
RESULT 542	
ID	ADE19544 standard; protein; 653 AA.
DE	Human PRO polypeptide #219.
PN	US2003199025-A1.
PD	23-OCT-2003.
PA	(GETH) GENENTECH INC.
Query Match	10.5%; Score 330; DB 7; Length 653;
Best Local Similarity	24.3%; Pred. No. 2.1e-12;
RESULT 543	
ID	ADE18992 standard; protein; 653 AA.
DE	Human PRO polypeptide #219.
PN	US2003199026-A1.
PD	23-OCT-2003.
PA	(GETH) GENENTECH INC.
Query Match	10.5%; Score 330; DB 7; Length 653;
Best Local Similarity	24.3%; Pred. No. 2.1e-12;
RESULT 544	
ID	ADE43188 standard; protein; 653 AA.
DE	Human PRO polypeptide #219.
PN	US2003199033-A1.
PD	23-OCT-2003.
PA	(GETH) GENENTECH INC.
Query Match	10.5%; Score 330; DB 7; Length 653;
Best Local Similarity	24.3%; Pred. No. 2.1e-12;
RESULT 545	
ID	ADD95977 standard; protein; 653 AA.
DE	Human PRO polypeptide #219.
PN	US2003199059-A1.
PD	23-OCT-2003.
PA	(GETH) GENENTECH INC.
Query Match	10.5%; Score 330; DB 7; Length 653;
Best Local Similarity	24.3%; Pred. No. 2.1e-12;
RESULT 546	
ID	ADE22863 standard; protein; 653 AA.
DE	Human PRO polypeptide #219.
PN	US2003199064-A1.
PD	23-OCT-2003.
PA	(GETH) GENENTECH INC.
Query Match	10.5%; Score 330; DB 7; Length 653;
Best Local Similarity	24.3%; Pred. No. 2.1e-12;
RESULT 547	
ID	ADD78981 standard; protein; 653 AA.
DE	Human PRO polypeptide #219.
PN	US2003203429-A1.
PD	30-OCT-2003.
PA	(GETH) GENENTECH INC.
Query Match	10.5%; Score 330; DB 7; Length 653;
Best Local Similarity	24.3%; Pred. No. 2.1e-12;
RESULT 548	
ID	ADE26219 standard; protein; 653 AA.
DE	Novel human secreted and transmembrane protein PROI111.
PN	US2003087305-A1.
PD	08-MAY-2003.
PA	(GETH) GENENTECH INC.
Query Match	10.5%; Score 330; DB 7; Length 653;
Best Local Similarity	24.3%; Pred. No. 2.1e-12;
RESULT 549	
ID	ADE32931 standard; protein; 653 AA.
DE	Novel human secreted and transmembrane protein PROI111.
PN	US2003194766-A1.
PD	16-OCT-2003.
PA	(GETH) GENENTECH INC.
Query Match	10.5%; Score 330; DB 7; Length 653;
Best Local Similarity	24.3%; Pred. No. 2.1e-12;
RESULT 550	
ID	ADE42623 standard; protein; 653 AA.
DE	Human PRO polypeptide #219.
PN	US2003199032-A1.

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Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 551
ID ADG80628 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 552
ID ADG89667 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 553
ID ADE40951 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 554
ID ADE04750 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 555
ID ADE92879 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 556
ID ADF67156 standard; protein; 653 AA.
DE Human PRO1111 amino acid sequence SEQ ID NO:229.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 557
ID ADG21588 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 558
ID ADG23229 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 559
ID ADP97564 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 560
ID ADG80628 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 561
ID ADG80076 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 562
ID ADH55368 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 563
ID ADH55920 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 564
ID ADI35410 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 565
ID ADI64139 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 566
ID ADI65088 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 567
ID ADI63587 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 568
ID ADH82001 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 569
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
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ID ADH99902 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 570
ID ADH81449 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 571
ID ADM26218 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 572
ID ADN16017 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 573
ID ADN16646 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 574
ID ADN15465 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 575
ID ADN14913 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 576
ID ADC81175 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 577
ID ADD76623 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 578
ID ADD87987 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199054-A1.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 579
ID ADH66391 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 580
ID ADE75839 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 581
ID ADE23415 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 582
ID ADE23967 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 583
ID ADE24610 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 584
ID ADH7435 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 585
ID ADE89301 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 586
ID ADE18440 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 587
ID ADE88749 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199054-A1.
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Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 606
ID ADG16824 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 607
ID ADG05283 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 608
ID ADG19550 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 609
ID ADG13387 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 610
ID ADG08444 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 611
ID ADG15614 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 612
ID ADF97012 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 613
ID ADG06197 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 614
ID ADG21781 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 615
ID ADG04070 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 616
ID ADG24971 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 617
ID ADG07268 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 618
ID ADG07820 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 619
ID ADG5315 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 620
ID ADG60979 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 621
ID ADG62083 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 622
ID ADG82284 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 623
ID ADG57523 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 624
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ID ADG56971 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 625
ID ADG55867 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 626
ID ADG58627 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 627
ID ADG70993 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 628
ID ADG58075 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 629
ID ADG53659 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 630
ID ADG71545 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 631
ID ADG81732 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 632
ID ADH19475 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 633
ID ADH30694 standard; protein; 653 AA.
DE Human PRO polypeptide #219.

PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 634
ID ADH12061 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 635
ID ADG52483 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 636
ID ADG54211 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 637
ID ADG81180 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 638
ID ADG56419 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 639
ID ADH12685 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 640
ID ADH20968 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003224358-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 641
ID ADG61531 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 642
ID ADH20008 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003219856-A1.
PD 27-NOV-2003.

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PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 643
ID ADH28618 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 644
ID ADG54763 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 645
ID ADG59803 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 646
ID ADI81227 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 647
ID ADG09970 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 648
ID ADI15441 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 649
ID ADG09318 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 650
ID ADI14773 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 651
ID ADI18368 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 652
ID ADJ63649 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US20040319164-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 653
ID ADJ77544 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 654
ID ADJ65666 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 655
ID ADM27802 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 656
ID ADM42526 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 657
ID ADM28388 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 658
ID ADI95870 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 659
ID ADI96422 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 660
ID ADS32374 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2004203125-A1.
PD 14-OCT-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
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Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 661
ID ADT03358 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2004214269-A1.
PD 28-OCT-2004.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 662
ID ADZ03409 standard; protein; 653 AA.
DE Human secreted/transmembrane PRO1111 protein.
PN US2005074837-A1.
PD 07-APR-2005.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 9; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 663
ID AEA38492 standard; protein; 653 AA.
DE Human secreted/transmembrane protein, #132.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 9; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 664
ID AEA23332 standard; protein; 653 AA.
DE Tumor antigen of hematopoietic origin TAHO15.
PN WO2005049075-A2.
PD 02-JUN-2005.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 9; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 665
ID AEB14155 standard; protein; 653 AA.
DE Cancer cell diagnosis method-related human protein - SEQ ID 438.
PN US2005153396-A1.
PD 14-JUL-2005.
PA (BAKE/) BAKER K P.
PA (BERE/) BERESINI M.
PA (DERO/) DEFORGE L.
PA (DESN/) DESNOYERS L.
PA (FILV/) FILVAROFF E.
PA (GAOW/) GAO W.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (SHER/) SHERWOOD S.
PA (SMIT/) SMITH V.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
Query Match 10.5%; Score 330; DB 9; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 666
ID ABU12069 standard; protein; 775 AA.
DE Human NOV15a CG92531-01 protein SEQ ID 58.
PN WO200281625-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 10.5%; Score 329.5; DB 6; Length 775;
Best Local Similarity 26.0%; Pred. No. 2.8e-12;
RESULT 667
ID ABG98014 standard; protein; 649 AA.
DE Human leucine rich repeat domain protein associated protein #1.
PN WO200274959-A2.
PD 26-SEP-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 10.5%; Score 329; DB 5; Length 649;
Best Local Similarity 24.6%; Pred. No. 2.5e-12;

RESULT 668
ID ADS98753 standard; protein; 824 AA.
DE Protein factor discovery related human contig polypeptide, SEQ ID 1017.
PN WO2004087874-A2.
PD 14-OCT-2004.
PA (NUVE-) NUVELO INC.
PA (DRMA/) DRMANAC R T.
Query Match 10.5%; Score 329; DB 8; Length 824;
Best Local Similarity 25.5%; Pred. No. 3.3e-12;
RESULT 669
ID AEG34079 standard; protein; 627 AA.
DE Human Pro peptide #51.
PN WO200224888-A2.
PD 28-MAR-2002.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 5; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 670
ID ADA01368 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003068779-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 6; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 671
ID ADA43797 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003064474-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 6; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 672
ID ADA43565 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003073196-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 6; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 673
ID ADA01240 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003068782-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 6; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 674
ID ADA01124 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003068780-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 675
ID ADA43681 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003073190-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 676
ID ADA06943 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003068781-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;

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RESULT 677
ID ADA08431 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003068783-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 678
ID ADB99724 standard; protein; 627 AA.
DE Human PRO polypeptide SEQ ID 100.
PN US2003082728-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 679
ID ADB87007 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003082726-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 680
ID ADB66162 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003082729-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 681
ID ADB99840 standard; protein; 627 AA.
DE Human PRO polypeptide SEQ ID 100.
PN US2003073192-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 682
ID ADB99495 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003082731-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 683
ID ADB66046 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003082732-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 684
ID ADC23444 standard; protein; 627 AA.
DE Human transmembrane PRO polypeptide (SeqID 100).
PN US2003073193-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 685
ID ADC26137 standard; protein; 627 AA.
DE Human PRO34192 protein.
PN US2003073194-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 686
ID ADA04964 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003068778-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 687
ID ADE11270 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003073191-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 688
ID ADD88201 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003082733-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 689
ID ADD95496 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003064473-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 690
ID ADE06426 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003073195-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 691
ID ADE38201 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119120-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 692
ID ADD88317 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003073189-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 693
ID ADD90898 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003073188-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 694
ID ADF99453 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003078401-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 695
ID ADG06546 standard; protein; 627 AA.
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DE Human PRO polypeptide #50.
PN US2003077742-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 696
ID ADG03497 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003077741-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 697
ID ADG82498 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003077744-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 698
ID ADE51751 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003104560-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 699
ID ADE51867 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003104561-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 700
ID ADE37725 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003104584-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 701
ID ADE37609 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003104565-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 702
ID ADD95380 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003138901-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 703
ID ADE38080 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003104566-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 704
ID ADE76169 standard; protein; 627 AA.
DE Human PRO polypeptide #50.

PN US2003124665-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 705
ID ADE39492 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119117-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 706
ID ADE04296 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003096364-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 707
ID ADE39893 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003138996-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 708
ID ADE19758 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003138903-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 709
ID ADE77336 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003124666-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 710
ID ADE65444 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119116-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 711
ID ADE76053 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003124663-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 712
ID ADE37964 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119119-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 713
ID ADE64574 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119114-A1.

PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 714
ID ADE38909 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003096363-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 715
ID ADE31983 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003104562-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 716
ID ADD91014 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003138902-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 717
ID ADE38793 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003108996-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 718
ID ADE37493 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003104563-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 719
ID ADE06309 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003138898-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 720
ID ADD90169 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003138904-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 721
ID ADE38677 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119086-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 722
ID ADE39608 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119118-A1.
PD 26-JUN-2003.

PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 723
ID ADD89213 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003138897-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 724
ID ADD88980 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003138899-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 725
ID ADE19874 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003138900-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 726
ID ADE77452 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003124667-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 727
ID ADE65328 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119113-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 728
ID ADE39376 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119115-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 729
ID ADE38561 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003104559-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 730
ID ADG11114 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003170809-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 731
ID ADG10998 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003077743-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 732
ID ADH31526 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119139-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 733
ID ADH38774 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003119140-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 734
ID ADH29409 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003119137-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 735
ID ADH23712 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003119143-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 736
ID ADH27042 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003119135-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 737
ID ADH38310 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119124-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 738
ID ADH26926 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003119134-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 739
ID ADH38194 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119123-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 740
ID ADH38890 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003119141-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;

Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 741
ID ADH23828 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003119142-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 742
ID ADH40203 standard; protein; 627 AA.
DE Human PRO34192 protein.
PN US2003119132-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 743
ID ADH40088 standard; protein; 627 AA.
DE Human PRO34192 protein.
PN US2003119133-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 744
ID ADH31410 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119138-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 745
ID ADH29288 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003119136-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 746
ID ADH49503 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119127-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 747
ID ADH51967 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119125-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 748
ID ADH49822 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119128-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 749
ID ADH52423 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119130-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;

RESULT 750
ID ADH52539 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119129-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 751
ID ADH58536 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119121-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 752
ID ADH51851 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119126-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 753
ID ADH58412 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119122-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 754
ID ADI13609 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119131-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 755
ID ADK00865 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003186373-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 756
ID ADL08606 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003186372-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 757
ID AAU32870 standard; protein; 636 AA.
DE Novel human secreted protein #3361.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.4%; Score 327.5; DB 4; Length 636;
Best Local Similarity 24.2%; Pred. No. 3e-12;
RESULT 758
ID ABO84499 standard; protein; 626 AA.
DE Mouse cancer-associated protein MP14-035.1.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 10.3%; Score 324; DB 8; Length 626;
Best Local Similarity 24.3%; Pred. No. 4.9e-12;
RESULT 759
ID AAG5805 standard; protein; 628 AA.
DE Human leucine-rich repeat (LRR) family member, 33395 polypeptide.
PN WO200172827-A2.
PD 04-OCT-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.3%; Score 324; DB 4; Length 628;
Best Local Similarity 24.1%; Pred. No. 4.9e-12;
RESULT 760
ID ADN95165 standard; protein; 810 AA.
DE Human BEC/LEC-related protein sequence SeqID87.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 10.3%; Score 322.5; DB 7; Length 810;
Best Local Similarity 22.0%; Pred. No. 8.2e-12;
RESULT 761
ID ABR58642 standard; protein; 811 AA.
DE Human cancer related protein SEQ ID NO:299.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 10.3%; Score 322.5; DB 6; Length 811;
Best Local Similarity 22.0%; Pred. No. 8.3e-12;
RESULT 762
ID AAO23114 standard; protein; 811 AA.
DE KIAA0644 'human modifier of p53 pathway' protein.
PN WO2003035833-A2.
PD 01-MAY-2003.
PA (EXEL-) EXELIXIS INC.
Query Match 10.3%; Score 322.5; DB 6; Length 811;
Best Local Similarity 22.0%; Pred. No. 8.3e-12;
RESULT 763
ID ADN95110 standard; protein; 811 AA.
DE Human LEC protein sequence SeqID32.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 10.3%; Score 322.5; DB 7; Length 811;
Best Local Similarity 22.0%; Pred. No. 8.3e-12;
RESULT 764
ID ADQ21196 standard; protein; 811 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 4016.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 10.3%; Score 322.5; DB 8; Length 811;
Best Local Similarity 22.0%; Pred. No. 8.3e-12;
RESULT 765
ID ADR45590 standard; protein; 605 AA.
DE Homologue of LRSG-1, baboon ALS.
PN US2004176296-A1.
PD 09-SEP-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.3%; Score 322; DB 8; Length 605;
Best Local Similarity 36.2%; Pred. No. 6.3e-12;
RESULT 766
ID AAG67523 standard; protein; 628 AA.
DE Amino acid sequence of a human secreted polypeptide.
PN WO200166690-A2.
PD 13-SEP-2001.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 10.2%; Score 321; DB 4; Length 628;
Best Local Similarity 23.9%; Pred. No. 7.6e-12;
RESULT 767
ID AAB84469 standard; protein; 628 AA.
DE Amino acid sequence of an interferon omega-1 like protein NOV2.
PN WO200142471-A2.
PD 14-JUN-2001.
PA (CURA-) CURAGEN CORP.
Query Match 10.2%; Score 321; DB 4; Length 628;

Best Local Similarity 23.9%; Pred. No. 7.6e-12;
RESULT 768
ID ABP69326 standard; protein; 628 AA.
DE Human polypeptide SEQ ID NO 1373.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 10.2%; Score 321; DB 5; Length 628;
Best Local Similarity 23.9%; Pred. No. 7.6e-12;
RESULT 769
ID ADF69107 standard; protein; 628 AA.
DE Human MP53 protein sequence SEQ ID NO:77.
PN WO2003083047-A2.
PD 09-OCT-2003.
PA (EXEL-) EXELIXIS INC.
Query Match 10.2%; Score 321; DB 7; Length 628;
Best Local Similarity 23.9%; Pred. No. 7.6e-12;
RESULT 770
ID ADH71652 standard; protein; 628 AA.
DE Human protein of the invention NOV22a SEQ ID NO:548.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 10.2%; Score 321; DB 8; Length 628;
Best Local Similarity 23.9%; Pred. No. 7.6e-12;
RESULT 771
ID ADH71654 standard; protein; 628 AA.
DE Human protein of the invention NOV22b SEQ ID NO:550.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 10.2%; Score 321; DB 8; Length 628;
Best Local Similarity 23.9%; Pred. No. 7.6e-12;
RESULT 772
ID ABO84502 standard; protein; 628 AA.
DE Human cancer-associated protein HP14-035.3.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 10.2%; Score 321; DB 8; Length 628;
Best Local Similarity 23.9%; Pred. No. 7.6e-12;
RESULT 773
ID ABO84503 standard; protein; 628 AA.
DE Human cancer-associated protein HP14-035.4.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 10.2%; Score 321; DB 8; Length 628;
Best Local Similarity 23.9%; Pred. No. 7.6e-12;
RESULT 774
ID ABO84501 standard; protein; 628 AA.
DE Human cancer-associated protein HP14-035.2.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 10.2%; Score 321; DB 8; Length 628;
Best Local Similarity 23.9%; Pred. No. 7.6e-12;
RESULT 775
ID ABP70928 standard; protein; 762 AA.
DE Human LP341 protein.
PN WO2003029778-A2.
PD 10-APR-2003.
PA (ELLIL) LILLY & CO ELI.
Query Match 10.2%; Score 321; DB 6; Length 762;
Best Local Similarity 25.5%; Pred. No. 9.6e-12;
RESULT 776
ID ADI36917 standard; protein; 797 AA.
DE Human LRR protein #12.
PN US2003220263-A1.
PD 27-NOV-2003.
PA (FEDE/) FEDER J N.
PA (MINT/) MINTIER G.
PA (RAMA/) RAMANATHAN C S.

Query Match 10.2%; Score 321; DB 8; Length 797;
Best Local Similarity 25.5%; Pred. No. 1e-11;
RESULT 777
ID ADS98018 standard; protein; 803 AA.
DE Protein factor discovery related isolated human polypeptide, SEQ ID 282.
PN WO2004087874-A2.
PD 14-OCT-2004.
PA (NUVE-) NUVELO INC.
PA (DRMA/) DRMANAC R T.
Query Match 10.2%; Score 321; DB 8; Length 803;
Best Local Similarity 25.5%; Pred. No. 1e-11;
RESULT 778
ID AAY13349 standard; protein; 660 AA.
DE Amino acid sequence of protein PRO265.
PN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 2; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 779
ID ADC78348 standard; protein; 660 AA.
DE Human PRO265 protein.
PN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 3; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 780
ID AAB80217 standard; protein; 660 AA.
DE Human PRO285 protein.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 4; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 781
ID AAB31208 standard; protein; 660 AA.
DE Amino acid sequence of human polypeptide PRO265.
PN WO200077037-A2.
PD 21-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 4; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 782
ID AAU12346 standard; protein; 660 AA.
DE Human PRO265 polypeptide sequence.
PN WO200140468-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 4; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 783
ID ABB84839 standard; protein; 660 AA.
DE Human PRO285 protein sequence SEQ ID NO:46.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 5; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 784
ID ABB95445 standard; protein; 660 AA.
DE Human angiogenesis related protein PRO265 SEQ ID NO: 46.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M B.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.

PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 10.2%; Score 320; DB 5; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 785
ID ABU71595 standard; protein; 660 AA.
DE Human PRO polypeptide #6.
PN US2002146709-A1.
PD 13-FEB-2003.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 786
ID ABO17790 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003032156-A1.
PD 13-FEB-2003.
PD (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 787
ID ABU71450 standard; protein; 660 AA.
DE Human PRO polypeptide #6.
PN US2002192659-A1.
PD 19-DEC-2002.
PD (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 788
ID ABO25179 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003040014-A1.
PD 27-FEB-2003.
PD (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 789
ID ABU81044 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003004311-A1.
PD 02-JAN-2003.
PD (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 790
ID ABU71896 standard; protein; 660 AA.
DE Human secreted/transmembrane protein PRO265.
PN US2003003530-A1.
PD 02-JAN-2003.
PD (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 791
ID ABO01779 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2002157671-A1.
PD 26-DEC-2002.
PD (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 792
ID ABU66744 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003036180-A1.
PD 20-FEB-2003.
PD (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 793
ID ABU54352 standard; protein; 660 AA.
DE Human secreted/transmembrane protein PRO265.
PN US2002132240-A1.
PD 19-SEP-2002.
PD (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 794
ID ABU67297 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003032063-A1.
PD 13-FEB-2003.
PD (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 795
ID AAO23116 standard; protein; 660 AA.
DE FLRT2 'human modifier of p53 pathway' protein.
PN WO2003035833-A2.
PD 01-MAY-2003.
PD (EXEL-) EXELIXIS INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 796
ID ABO47367 standard; protein; 660 AA.
DE Human secreted/transmembrane polypeptide PRO265.
PN US2003044839-A1.
PD 06-MAR-2003.
PD (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 797
ID ABUS9825 standard; protein; 660 AA.
DE Novel secreted and transmembrane protein PRO265.
PN US2003017563-A1.
PD 23-JAN-2003.
PD (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 798
ID ABO25015 standard; protein; 660 AA.
DE Human secreted/transmembrane protein (PRO) #175.
PN US2003036179-A1.
PD 20-FEB-2003.
PD (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 799
ID ABU64504 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2002160374-A1.
PD 31-OCT-2002.
PD (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 800
ID ABU72065 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US200217165-A1.
PD 28-NOV-2002.
PD (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 801
ID ABU67350 standard; protein; 660 AA.
DE Human secreted protein PRO265.
PN US2003023054-A1.
PD 30-JAN-2003.
PD (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 802

ID ABU67166 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003032062-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 803
ID ABO14870 standard; protein; 660 AA.
DE Human secreted / transmembrane polypeptide PRO265.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 804
ID ABU67020 standard; protein; 660 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 350.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 805
ID ABU69627 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 806
ID ABU79808 standard; protein; 660 AA.
DE Human secreted/transmembrane protein PRO265.
PN US2003032057-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 807
ID ABO14809 standard; protein; 660 AA.
DE Human secreted / transmembrane polypeptide PRO265.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 808
ID ADA45869 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 809
ID ADA76300 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 810
ID ADB23233 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 811
ID ADA18950 standard; protein; 660 AA.

DE Human PRO polypeptide #175.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 812
ID ADA61573 standard; protein; 660 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 813
ID ADB19358 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 814
ID ADB27899 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 815
ID ADA86378 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 816
ID ADB15942 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 817
ID ADA47728 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 818
ID ADA18089 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 819
ID ABO32761 standard; protein; 660 AA.
DE Human secreted/transmembrane protein PRO265.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 820
ID ADA67523 standard; protein; 660 AA.

PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 821
ID ADB30530 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 822
ID ADA5826 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 823
ID ADA97038 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 824
ID ADA79342 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 825
ID ADA87481 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 826
ID ADB16683 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 827
ID ABO34821 standard; protein; 660 AA.
DE Human PRO polypeptide #6.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 828
ID ADA16064 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 829
ID ADA91775 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082694-A1.

PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 830
ID ADB14838 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 831
ID ADA47287 standard; protein; 660 AA.
DE Human secreted/transmembrane polypeptide PRO265.
PN US2003044844-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 832
ID ADB18799 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 833
ID ADA94014 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 834
ID ADB19910 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 835
ID ADB13222 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 836
ID ABO43323 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 837
ID ADA74476 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 838
ID ADA42209 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003054401-A1.
PD 20-MAR-2003.


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Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 857
ID ADA95934 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 858
ID ADB26243 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 859
ID ADB21728 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 860
ID ADA77507 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 861
ID ADB18247 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 862
ID ADA96930 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 863
ID ADA16488 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 864
ID ADA12917 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 865
ID ADA41785 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 866
ID ADA88033 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 867
ID ADA46421 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 868
ID ADA17132 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 869
ID ADA42635 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 870
ID ADB28451 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 871
ID ADB29003 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 872
ID ADA76955 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 873
ID ADA88585 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 874
ID ADA97590 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082886-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 875
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ID ADB27347 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003022239-A1.
PD 30-JAN-2003.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 876
ID ADB22280 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087344-A1.
PD 08-MAY-2003.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 877
ID ABO19866 standard; protein; 660 AA.
DE Human secreted/transmembrane protein PRO265.
PN US2003044902-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 878
ID ABO17560 standard; protein; 660 AA.
DE Human PRO polypeptide #6.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 879
ID ADA66971 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 880
ID ADB22832 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 881
ID ADB23605 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 882
ID ADA92327 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 883
ID ADB15390 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 884
ID ADB38642 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082766-A1.
PD 01-MAY-2003.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 885
ID ADB38090 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 886
ID ADB66562 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 887
ID ADB89642 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 888
ID ADB90374 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 889
ID ADB77554 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 890
ID ADB39475 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 891
ID ADB74690 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 892
ID ADB47098 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 893
ID ADB86705 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082697-A1.
PD 01-MAY-2003.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 894
ID ADB86705 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082697-A1.
PD 01-MAY-2003.

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PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 894
ID ADB77310 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO365.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 895
ID ADB34467 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US2003077117-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 896
ID ADB35571 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US2003077119-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 897
ID ADB33915 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US2003077116-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 898
ID ADB35019 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US2003077118-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 899
ID ADB36123 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US200307720-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 900
ID ADB46518 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO365.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 901
ID ADC28336 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 902
ID ADC39536 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 903
ID ADC40050 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 904
ID ADC18878 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 905
ID ADC34174 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 906
ID ADC29229 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 907
ID ADC28760 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 908
ID ADC40645 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 909
ID ADC19302 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 910
ID ADC33750 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 911
ID ADC12820 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
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Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 912
ID ADC50391 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 913
ID ADC71938 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 914
ID ADC59917 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 915
ID ADC52924 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein Seq ID350.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 916
ID ADC57278 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein Seq ID350.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 917
ID ADC60469 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 918
ID ADC50944 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 919
ID ADC65471 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 920
ID ADC54569 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein Seq ID350.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 921
ID ADC53530 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein Seq ID350.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 922
ID ADC59053 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein Seq ID350.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 923
ID ADC55931 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein Seq ID350.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 924
ID ADC58501 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein Seq ID350.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 925
ID ADC12272 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 926
ID ADD03175 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 927
ID ADC90167 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 928
ID ADC69586 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 929
ID ADC48475 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 930
ID ADC50391 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.

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ID ADD10004 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 931
ID ADD04579 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 932
ID ADC080535 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 933
ID ADD11042 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 934
ID ADD10335 standard; protein; 660 AA.
DE Human secreted/transmembrane PRO polypeptide #23.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 935
ID ADC47923 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 936
ID ADD04827 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 937
ID ADC79983 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 938
ID ADD11295 standard; protein; 660 AA.
DE Human secreted/transmembrane PRO polypeptide #23.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 939
ID ADD09452 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 940
ID ADD03833 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 941
ID ADD03409 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 942
ID ADD41165 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 943
ID ADD52304 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 944
ID ADD53044 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 945
ID ADD53596 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 946
ID ADD37088 standard; protein; 660 AA.
DE Human secreted/transmembrane PRO polypeptide #23.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 947
ID ADD51752 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 948
ID ADD02551 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
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PD US2003203431-A1.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 949
ID ADD01985 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 950
ID ADD54167 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 951
ID ADD92484 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 952
ID ADD91380 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199035-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 953
ID ADE03994 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 954
ID ADE32291 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 955
ID ADE22223 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 956
ID ADD79447 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 957
ID ADE41983 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194772-A1.

PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 958
ID ADE17800 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 959
ID ADD91932 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 960
ID ADE33395 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 961
ID ADE33947 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 962
ID ADD79999 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 963
ID ADD93036 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 964
ID ADE19456 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 965
ID ADE34661 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 966
ID ADE18904 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199026-A1.
PD 23-OCT-2003.

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PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 967
ID ADE43100 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 968
ID ADD95889 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 969
ID ADE22775 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 970
ID ADD78893 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 971
ID ADE32843 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003194786-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 972
ID ADE42535 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 973
ID ADD80551 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 974
ID ADD89579 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 975
ID ADE40863 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 976
ID ADE04662 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 977
ID ADE92791 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 978
ID ADG21500 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 979
ID ADG23141 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 980
ID ADF97476 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 981
ID ADG80540 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 982
ID ADG79988 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 983
ID ADG63796 standard; protein; 660 AA.
DE Human secreted/transmembrane polypeptide PRO265.
PN US2003170721-A1.
PD 11-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 984
ID ADH59144 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
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Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 985
ID ADH55280 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 986
ID ADH55832 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 987
ID ADI37923 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 988
ID ADI65000 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 989
ID ADI63499 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 990
ID ADH81913 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 991
ID ADH81361 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 992
ID ADJ26191 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 993
ID ADM82530 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 994
ID ADNI5929 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 995
ID ADNI6558 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 996
ID ADNI5377 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 997
ID ADNI4825 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 998
ID ADI64051 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 999
ID ADC81087 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1000
ID ADE79106 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1001
ID ADD76535 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1002
ID ADD87899 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1003
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PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
  RESULT 1022
  ID ADF34924 standard; protein; 660 AA.
  DE Human PRO polypeptide #175.
  PN US2003199029-A1.
  PD 23-OCT-2003.
  PA (GETH ) GENENTECH INC.
    Query Match 10.2%; Score 320; DB 8; Length 660;
    Best Local Similarity 22.4%; Pred. No. 9.3e-12;
    RESULT 1023
    ID ADE98414 standard; protein; 660 AA.
    DE Human secreted/transmembrane protein, #7.
    PN US2003211569-A1.
    PD 13-NOV-2003.
    PA (GETH ) GENENTECH INC.
      Query Match 10.2%; Score 320; DB 8; Length 660;
      Best Local Similarity 22.4%; Pred. No. 9.3e-12;
      RESULT 1024
      ID ADE92239 standard; protein; 660 AA.
      DE Novel human secreted and transmembrane protein PRO265.
      PN US2003199051-A1.
      PD 23-OCT-2003.
      PA (GETH ) GENENTECH INC.
        Query Match 10.2%; Score 320; DB 8; Length 660;
        Best Local Similarity 22.4%; Pred. No. 9.3e-12;
        RESULT 1025
        ID ADE90540 standard; protein; 660 AA.
        DE Human PRO polypeptide #175.
        PN US2003199063-A1.
        PD 23-OCT-2003.
        PA (GETH ) GENENTECH INC.
          Query Match 10.2%; Score 320; DB 8; Length 660;
          Best Local Similarity 22.4%; Pred. No. 9.3e-12;
          RESULT 1026
          ID ADE91687 standard; protein; 660 AA.
          DE Novel human secreted and transmembrane protein PRO265.
          PN US2003199058-A1.
          PD 23-OCT-2003.
          PA (GETH ) GENENTECH INC.
            Query Match 10.2%; Score 320; DB 8; Length 660;
            Best Local Similarity 22.4%; Pred. No. 9.3e-12;
            RESULT 1027
            ID ADE98841 standard; protein; 660 AA.
            DE Human secreted/transmembrane protein, #7.
            PN US2003211569-A1.
            PD 13-NOV-2003.
            PA (GETH ) GENENTECH INC.
              Query Match 10.2%; Score 320; DB 8; Length 660;
              Best Local Similarity 22.4%; Pred. No. 9.3e-12;
              RESULT 1028
              ID ADG40311 standard; protein; 660 AA.
              DE Human secreted/transmembrane protein, #7.
              PN US2003225253-A1.
              PD 04-DEC-2003.
              PA (DESN/) DESNOYERS L.
              PA (GODD/) GODDARD A.
              PA (GODO/) GODOWSKI P J.
              PA (GURN/) GURNEY A L.
              PA (MATH/) MATHER J P.
              PA (WILL/) WILLIAMS P M.
              PA (WOOD/) WOOD W I.
            Query Match 10.2%; Score 320; DB 8; Length 660;
            Best Local Similarity 22.4%; Pred. No. 9.3e-12;
            RESULT 1029
            ID ADF73705 standard; protein; 660 AA.
            DE Human secreted/transmembrane protein, #7.
            PN US2003180312-A1.
            PD 25-SEP-2003.
            PA (GETH ) GENENTECH INC.
              Query Match 10.2%; Score 320; DB 8; Length 660;
              Best Local Similarity 22.4%; Pred. No. 9.3e-12;
              RESULT 1030
              ID ADG02266 standard; protein; 660 AA.
              DE Human PRO polypeptide #175.
              PN US2003207352-A1.
              PD 06-NOV-2003.
              PA (GETH ) GENENTECH INC.
                Query Match 10.2%; Score 320; DB 8; Length 660;
                Best Local Similarity 22.4%; Pred. No. 9.3e-12;
                RESULT 1031
                ID ADG22052 standard; protein; 660 AA.
                DE Novel human secreted and transmembrane protein PRO365.
                PN US2003207360-A1.
                PD 06-NOV-2003.
                PA (GETH ) GENENTECH INC.
                  Query Match 10.2%; Score 320; DB 8; Length 660;
                  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
                  RESULT 1032
                  ID ADG20122 standard; protein; 660 AA.
                  DE Human PRO polypeptide #175.
                  PN US2003207376-A1.
                  PD 06-NOV-2003.
                  PA (GETH ) GENENTECH INC.
                    Query Match 10.2%; Score 320; DB 8; Length 660;
                    Best Local Similarity 22.4%; Pred. No. 9.3e-12;
                    RESULT 1033
                    ID ADF98028 standard; protein; 660 AA.
                    DE Human PRO polypeptide #175.
                    PN US2003207422-A1.
                    PD 06-NOV-2003.
                    PA (GETH ) GENENTECH INC.
                      Query Match 10.2%; Score 320; DB 8; Length 660;
                      Best Local Similarity 22.4%; Pred. No. 9.3e-12;
                      RESULT 1034
                      ID ADG34245 standard; protein; 660 AA.
                      DE Novel human secreted and transmembrane protein PRO365.
                      PN US2003207426-A1.
                      PD 06-NOV-2003.
                      PA (GETH ) GENENTECH INC.
                        Query Match 10.2%; Score 320; DB 8; Length 660;
                        Best Local Similarity 22.4%; Pred. No. 9.3e-12;
                        RESULT 1035
                        ID ADF98599 standard; protein; 660 AA.
                        DE Human PRO polypeptide #175.
                        PN US2003208055-A1.
                        PD 06-NOV-2003.
                        PA (GETH ) GENENTECH INC.
                          Query Match 10.2%; Score 320; DB 8; Length 660;
                          Best Local Similarity 22.4%; Pred. No. 9.3e-12;
                          RESULT 1036
                          ID ADG03430 standard; protein; 660 AA.
                          DE Human PRO polypeptide #175.
                          PN US2003207351-A1.
                          PD 06-NOV-2003.
                          PA (GETH ) GENENTECH INC.
                            Query Match 10.2%; Score 320; DB 8; Length 660;
                            Best Local Similarity 22.4%; Pred. No. 9.3e-12;
                            RESULT 1037
                            ID ADF99151 standard; protein; 660 AA.
                            DE Human PRO polypeptide #175.
                            PN US2003207353-A1.
                            PD 06-NOV-2003.
                            PA (GETH ) GENENTECH INC.
                              Query Match 10.2%; Score 320; DB 8; Length 660;
                              Best Local Similarity 22.4%; Pred. No. 9.3e-12;
                              RESULT 1038
                              ID ADG16736 standard; protein; 660 AA.
                              DE Human PRO polypeptide #175.
                              PN US2003207359-A1.
                              PD 06-NOV-2003.
                              PA (GETH ) GENENTECH INC.
                                Query Match 10.2%; Score 320; DB 8; Length 660;
                                Best Local Similarity 22.4%; Pred. No. 9.3e-12;
                                RESULT 1039
                                ID ADF73705 standard; protein; 660 AA.
                                DE Human secreted/transmembrane protein, #7.
                                PN US2003180312-A1.
                                PD 25-SEP-2003.
                                PA (GETH ) GENENTECH INC.
                                  Query Match 10.2%; Score 320; DB 8; Length 660;
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Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1039
ID ADG05195 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1040
ID ADG19462 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1041
ID ADF73281 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1042
ID ADG13299 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1043
ID ADG08356 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1044
ID ADG15526 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1045
ID ADF96924 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1046
ID ADG06109 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1047
ID ADG23693 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1048
ID ADG03982 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1049
ID ADG24883 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1050
ID ADG07180 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1051
ID ADG07732 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1052
ID ADG55227 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1053
ID ADG60891 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1054
ID ADG61995 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1055
ID ADG92124 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1056
ID ADG82196 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1057
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ID ADG57435 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1058
ID ADG56883 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1059
ID ADG55779 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1060
ID ADG58539 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1061
ID ADG70905 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1062
ID ADG92551 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1063
ID ADG57987 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1064
ID ADG53571 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1065
ID ADG71457 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1066
ID ADG81644 standard; protein; 660 AA.

DE Human PRO polypeptide #175.
PN US2003207805-A1.
PD 06-NOV-2003.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1067
ID ADH30606 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1068
ID ADG63645 standard; protein; 660 AA.
DE Human secreted/transmembrane polypeptide PRO265.
PN US2003180796-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1069
ID ADH11973 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1070
ID ADG52395 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1071
ID ADG54123 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1072
ID ADG81092 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1073
ID ADG56331 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1074
ID ADH12597 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1075
ID ADG61443 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207429-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1076
ID ADH28530 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1077
ID ADG54675 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1078
ID ADG59715 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1079
ID ADH20340 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2004005533-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1080
ID ADH43479 standard; protein; 660 AA.
DE Human PRO polypeptide #23.
PN US2003224984-A1
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1081
ID ADH07195 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1082
ID ADH59740 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1083
ID ADH06768 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.

PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1084
ID ADI81139 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1085
ID ADI18510 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1086
ID ADI65230 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1087
ID ADI37493 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1088
ID ADG09882 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1089
ID ADH97297 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1090
ID ADI15353 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1091
ID ADG09230 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1092
ID ADI14685 standard; protein; 660 AA.

DE Novel human secreted and transmembrane protein PRO265.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1093
ID ADH60400 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHIER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1094
ID ADI18280 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1095
ID ADJ99457 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1096
ID ADL08650 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1097
ID ADM24995 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1098
ID ADJ63561 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1099
ID ADM29741 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1100
ID ADJ77456 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2004038336-A1.
PD 26-FEB-2004.

PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1101
ID ADK82824 standard; protein; 660 AA.
DE Human PRO polypeptide #23.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1102
ID ADJ65578 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1103
ID ADM27714 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1104
ID ADM42438 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1105
ID ADO06063 standard; protein; 660 AA.
DE Human PRO polypeptide #6.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1106
ID ADM28300 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1107
ID ADR10915 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1108
ID ADR17824 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.

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PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUNA/) TUNAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
  Query Match      10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1109
ID ADI95782 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003077659-A1
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1110
ID ADI96334 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1111
ID ADI65657 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1112
ID ADS74463 standard; protein; 660 AA.
DE Human secreted/transmembrane protein #7.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUNA/) TUNAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
  Query Match      10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1113
ID ADS32286 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2004203125-A1.
PD 14-OCT-2004.
PA (GETH ) GENENTECH INC.
  Query Match      10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1114
ID ADT03270 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2004214269-A1.
PD 28-OCT-2004.
PA (GETH ) GENENTECH INC.
  Query Match      10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1115
ID ADT03500 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH ) GENENTECH INC.
  Query Match      10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1116
ID ADU06386 standard; protein; 660 AA.
DE Novel bronchial cancer-associated human protein SeqID610.
PN DE10316701-A1.
PD 04-NOV-2004.
PA (HINZ/) HINZMANN B.
PA (HERM/) HERMANN K.
PA (CAST/) HEIDEN CASTANOS-VELEZ E.
  Query Match      10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1117
ID ADZ03321 standard; protein; 660 AA.
DE Human secreted/transmembrane PRO265 protein.
PN US2005074837-A1.
PD 07-APR-2005.
PA (GETH ) GENENTECH INC.
  Query Match      10.2%; Score 320; DB 9; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1118
ID AEA37738 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH ) GENENTECH INC.
  Query Match      10.2%; Score 320; DB 9; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1119
ID AEB14067 standard; protein; 660 AA.
DE Cancer cell diagnosis method-related human protein - SEQ ID 350.
PN US2005153396-A1.
PD 14-JUL-2005.
PA (BAKE/) BAKER K P.
PA (BERE/) BERESINI M.
PA (DEFO/) DEFOGE L.
PA (DESN/) DESNOYERS L.
PA (FILV/) FILVAROFF E.
PA (GROW/) GAO W.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (SHER/) SHERWOOD S.
PA (SMIT/) SMITH V.
PA (STEW/) STEWART T A.
PA (TUNA/) TUNAS D.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
  Query Match      10.2%; Score 320; DB 9; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
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RESULT 1120
 ID ADT77808 standard; protein; 452 AA.
 DE Chimeric Nogo receptor polypeptide.
 PN WO2004090103-A2.
 PD 21-OCT-2004.
 PA (UYRP) UNIV ROCHESTER.
 Query Match 10.2%; Score 318.5; DB 8; Length 452;
 Best Local Similarity 27.3%; Pred. No. 7.5e-12;
 RESULT 1121
 ID ADT77802 standard; protein; 452 AA.
 DE Chimeric Nogo receptor polypeptide.
 PN WO2004090103-A2.
 PD 21-OCT-2004.
 PA (UYRP) UNIV ROCHESTER.
 Query Match 10.2%; Score 318.5; DB 8; Length 452;
 Best Local Similarity 27.8%; Pred. No. 7.5e-12;
 RESULT 1122
 ID AAE13006 standard; protein; 713 AA.
 DE Human leucine-rich repeat (LRR) family member protein.
 PN WO200175105-A2.
 PD 11-OCT-2001.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 10.1%; Score 317.5; DB 4; Length 713;
 Best Local Similarity 23.1%; Pred. No. 1.5e-11;
 RESULT 1123
 ID AAU91335 standard; protein; 713 AA.
 DE Human novel secreted protein LP223(a).
 PN WO200214358-A2.
 PD 21-FEB-2002.
 PA (ELIL) LILLY & CO ELI.
 Query Match 10.1%; Score 316.5; DB 5; Length 713;
 Best Local Similarity 23.1%; Pred. No. 1.7e-11;
 RESULT 1124
 ID ABG97991 standard; protein; 713 AA.
 DE Human nervous system leucine rich repeat protein (HLRRNS1) #2.
 PN WO200274959-A2.
 PD 26-SEP-2002.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 Query Match 10.1%; Score 316.5; DB 5; Length 713;
 Best Local Similarity 23.1%; Pred. No. 1.7e-11;
 RESULT 1125
 ID ABUS2381 standard; protein; 713 AA.
 DE Human GPCR related protein NOV31a.
 PN WO200279398-A2.
 PD 10-OCT-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 10.1%; Score 316.5; DB 6; Length 713;
 Best Local Similarity 23.1%; Pred. No. 1.7e-11;
 RESULT 1126
 ID ADT77796 standard; protein; 474 AA.
 DE Chimeric Nogo receptor polypeptide.
 PN WO2004090103-A2.
 PD 21-OCT-2004.
 PA (UYRP) UNIV ROCHESTER.
 Query Match 10.0%; Score 314.5; DB 8; Length 474;
 Best Local Similarity 27.8%; Pred. No. 1.4e-11;
 RESULT 1127
 ID AAU91341 standard; protein; 656 AA.
 DE Human novel secreted protein LP223(b).
 PN WO200214358-A2.
 PD 21-FEB-2002.
 PA (ELIL) LILLY & CO ELI.
 Query Match 10.0%; Score 313.5; DB 5; Length 656;
 Best Local Similarity 23.6%; Pred. No. 2.4e-11;
 RESULT 1128
 ID ADL24097 standard; protein; 713 AA.
 DE Human NOVX polypeptide #71.
 PN US2004002120-A1.
 PD 01-JAN-2004.
 PA (KEKU/) KEKUDA R.
 PA (TCHH/) TCHERNEV V T.
 PA (LIUX/) LIU X.
 PA (SPYT/) SPYTEK K A.

PA (PATT/) PATTURAJAN M.
 PA (BURG/) BURGESS C E.
 PA (VERN/) VERNET C A M.
 PA (LILL/) LI L.
 PA (GORM/) GORMAN L.
 PA (MALI/) MALYANKAR U M.
 PA (BOLD/) BOLDOG F L.
 PA (GUOX/) GUO X.
 PA (SHEN/) SHENOY S G.
 PA (PADI/) PADIGARU M.
 PA (TAUP/) TAUPIER R J.
 PA (MILL/) MILLER C E.
 PA (CASM/) CASMAN S J.
 PA (PENA/) PENNA C E A.
 PA (GANG/) GANGOLLI E A.
 PA (GUSE/) GUSEV V Y.
 PA (SMIT/) SMITHSON G.
 PA (ZERR/) ZERHUSEN B D.
 PA (GERL/) GERLACH V.
 PA (POCH/) POCHART P F.
 PA (FERN/) FERNANDES E R.
 PA (SHIM/) SHIMKETS R A.
 PA (RAST/) RASTELLI L.
 PA (SPAD/) SPADERNA S K.
 PA (LARO/) LAROCHELLE W J.
 PA (ZHON/) ZHONG M.
 PA (KHRA/) KHRAMTSOV N V.
 PA (VOSS/) VOSS E Z.
 PA (HERR/) HERRMANN J L.
 Query Match 10.0%; Score 313.5; DB 8; Length 713;
 Best Local Similarity 23.1%; Pred. No. 2.6e-11;
 RESULT 1129
 ID AAE09437 standard; protein; 592 AA.
 DE Human sbgTango79a protein.
 PN WO200160850-A1.
 PD 23-AUG-2001.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 Query Match 10.0%; Score 312; DB 4; Length 592;
 Best Local Similarity 25.9%; Pred. No. 2.6e-11;
 RESULT 1130
 ID AAE25351 standard; protein; 592 AA.
 DE Human LP polypeptide, LP243.
 PN WO200248361-A2.
 PD 20-JUN-2002.
 PA (ELIL) LILLY & CO ELI.
 Query Match 10.0%; Score 312; DB 5; Length 592;
 Best Local Similarity 25.9%; Pred. No. 2.6e-11;
 RESULT 1131
 ID AAU91329 standard; protein; 592 AA.
 DE Human novel secreted protein LP243(b).
 PN WO200214358-A2.
 PD 21-FEB-2002.
 PA (ELIL) LILLY & CO ELI.
 Query Match 10.0%; Score 312; DB 5; Length 592;
 Best Local Similarity 25.9%; Pred. No. 2.6e-11;
 RESULT 1132
 ID ABP60996 standard; protein; 592 AA.
 DE Novel human protein. SEQ ID 83.
 PN WO200250105-A1.
 PD 27-JUN-2002.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (GLAX) GLAXO GROUP LTD.
 Query Match 10.0%; Score 312; DB 5; Length 592;
 Best Local Similarity 25.9%; Pred. No. 2.6e-11;
 RESULT 1133
 ID AAU79167 standard; protein; 592 AA.
 DE Human leucine-rich repeat proteins-like protein NOV4.
 PN WO200214358-A2.
 PD 21-FEB-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 10.0%; Score 312; DB 5; Length 592;
 Best Local Similarity 25.9%; Pred. No. 2.6e-11;

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Best Local Similarity 25.9%; Pred. No. 2.6e-11;
RESULT 1134
ID ABG74693 standard; protein; 592 AA.
DE Human CDD protein 6803363CD1 SEQ ID 19.
PN WO2003014322-A2.
PD 20-FEB-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 10.0%; Score 312; DB 6; Length 592;
Best Local Similarity 25.9%; Pred. No. 2.6e-11;
RESULT 1135
ID ADE03417 standard; protein; 592 AA.
DE Human immunoglobulin superfamily member BGS-2.
PN US2003195163-A1.
PD 16-OCT-2003.
PA (WUSS/) WU S.
PA (KRYSS/) KRYSTEK S R.
PA (LEEL/) LEE L.
PA (FEDE/) FEDER J N.
PA (CHEN/) CHENG J D.
Query Match 10.0%; Score 312; DB 7; Length 592;
Best Local Similarity 25.9%; Pred. No. 2.6e-11;
RESULT 1136
ID ADU02709 standard; protein; 592 AA.
DE Novel human polypeptide seqid 1176.
PN WO2004093804-A2.
PD 04-NOV-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 10.0%; Score 312; DB 8; Length 592;
Best Local Similarity 25.9%; Pred. No. 2.6e-11;
RESULT 1137
ID ABG61770 standard; protein; 608 AA.
DE Novel leucine-rich protein.
PN WO200229058-A2.
PD 11-APR-2002.
PA (CURA-) CURAGEN CORP.
Query Match 10.0%; Score 312; DB 5; Length 608;
Best Local Similarity 25.9%; Pred. No. 2.7e-11;
RESULT 1138
ID ABG97967 standard; protein; 634 AA.
DE Human nervous system leucine rich repeat protein (HLRRNS1) #1.
PN WO200274959-A2.
PD 26-SEP-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 9.9%; Score 311; DB 5; Length 634;
Best Local Similarity 24.1%; Pred. No. 3.3e-11;
RESULT 1139
ID ABR55628 standard; protein; 420 AA.
DE Amino acid sequence of rat Nogo-66 receptor homologue NgrH1.
PN WO2003035687-A1.
PD 01-MAY-2003.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS PHARMA GMBH.
Query Match 9.9%; Score 310.5; DB 6; Length 420;
Best Local Similarity 29.8%; Pred. No. 2.2e-11;
RESULT 1140
ID ADT77788 standard; protein; 420 AA.
DE Rat Nogo receptor 2 polypeptide.
PN WO2004090103-A2.
PD 21-OCT-2004.
PA (UYRP) UNIV ROCHESTER.
Query Match 9.9%; Score 310.5; DB 8; Length 420;
Best Local Similarity 29.8%; Pred. No. 2.2e-11;
RESULT 1141
ID AAO23115 standard; protein; 674 AA.
DE FLRT1 'human modifier of p53 pathway' protein.
PN WO2003035833-A2.
PD 01-MAY-2003.
PA (EXEL-) EXELIXIS INC.
Query Match 9.9%; Score 310.5; DB 6; Length 674;
Best Local Similarity 21.5%; Pred. No. 3.8e-11;
RESULT 1142
ID ADH17606 standard; protein; 674 AA.
DE Human NOV19a protein - SEQ ID 296.
PN WO200116318-A2.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.9%; Score 310.5; DB 8; Length 674;
Best Local Similarity 21.5%; Pred. No. 3.8e-11;
RESULT 1143
ID ADH17628 standard; protein; 674 AA.
DE Human NOV19l protein - SEQ ID 318.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.9%; Score 310.5; DB 8; Length 674;
Best Local Similarity 21.5%; Pred. No. 3.8e-11;
RESULT 1144
ID ADH17630 standard; protein; 674 AA.
DE Human NOV19m protein - SEQ ID 320.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.9%; Score 310.5; DB 8; Length 674;
Best Local Similarity 21.5%; Pred. No. 3.8e-11;
RESULT 1145
ID ADH17634 standard; protein; 674 AA.
DE Human NOV19o protein - SEQ ID 324.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.9%; Score 310.5; DB 8; Length 674;
Best Local Similarity 21.5%; Pred. No. 3.8e-11;
RESULT 1146
ID ADH17632 standard; protein; 674 AA.
DE Human NOV19n protein - SEQ ID 322.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.9%; Score 310.5; DB 8; Length 674;
Best Local Similarity 21.5%; Pred. No. 3.8e-11;
RESULT 1147
ID ABO27346 standard; protein; 585 AA.
DE Human secreted/transmembrane polypeptide PRO1865.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 585;
Best Local Similarity 22.3%; Pred. No. 4e-11;
RESULT 1148
ID ABO34232 standard; protein; 585 AA.
DE Human secreted/transmembrane polypeptide PRO 1865.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 585;
Best Local Similarity 22.3%; Pred. No. 4e-11;
RESULT 1149
ID AAU29215 standard; protein; 649 AA.
DE Human PRO polypeptide sequence #192.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 4; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1150
ID AAB70533 standard; protein; 649 AA.
DE Human PRO3 protein sequence SEQ ID NO:6.
PN WO200110902-A2.
PD 15-FEB-2001.
PA (CURA-) CURAGEN CORP.
Query Match 9.9%; Score 309; DB 4; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1151
ID AAB87591 standard; protein; 649 AA.
DE Human PRO1865.
PN WO200116318-A2.
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PD 08-MAR-2001.
 PA (GETH) GENENTECH INC.
 Query Match 9.9%; Score 309; DB 4; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.6e-11;
 RESULT 1152
 ID ABG95916 standard; protein; 649 AA.
 DE Human secreted/transmembrane protein PRO1865.
 PN US2002119130-A1.
 PD 29-AUG-2002.
 PA (GETH) GENENTECH INC.
 Query Match 9.9%; Score 309; DB 5; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.6e-11;
 RESULT 1153
 ID ABB84953 standard; protein; 649 AA.
 DE Human PRO1865 protein sequence SEQ ID NO:274.
 PN WO200200690-A2.
 PD 03-JAN-2002.
 PA (GETH) GENENTECH INC.
 Query Match 9.9%; Score 309; DB 5; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.6e-11;
 RESULT 1154
 ID ABP70109 standard; protein; 649 AA.
 DE Human NOV27a.
 PN WO200272771-A2.
 PD 19-SEP-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 9.9%; Score 309; DB 5; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.6e-11;
 RESULT 1155
 ID ABB95559 standard; protein; 649 AA.
 DE Human angiogenesis related protein PRO1865 SEQ ID NO: 274.
 PN WO200208284-A2.
 PD 31-JAN-2002.
 PA (GETH) GENENTECH INC.
 PA (BAKE/) BAKER K P.
 PA (FERR/) FERRARA N.
 PA (GERB/) GERBER H.
 PA (GERR/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (MARS/) MARSTERS S A.
 PA (PANJ/) PAN J.
 PA (PAON/) PAONI N F.
 PA (STEP/) STEPHAN J F.
 PA (WATA/) WATANABE C K.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 Query Match 9.9%; Score 309; DB 5; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.6e-11;
 RESULT 1156
 ID ABUS8591 standard; protein; 649 AA.
 DE Human PRO polypeptide #192.
 PN US2003027272-A1.
 PD 06-FEB-2003.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.6e-11;
 RESULT 1157
 ID ABUS88139 standard; protein; 649 AA.
 DE Novel human secreted and transmembrane protein PRO1865.
 PN US2003032127-A1.
 PD 13-FEB-2003.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.6e-11;
 RESULT 1158
 ID ABUS84454 standard; protein; 649 AA.
 DE Human secreted/transmembrane protein (PRO) #192.
 PN US2003032112-A1.
 PD 13-FEB-2003.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.6e-11;
 RESULT 1159
 ID ABR75034 standard; protein; 649 AA.
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
 PN US2003040056-A1.

ID ABR66328 standard; protein; 649 AA.
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
 PN US2003027278-A1.
 PD 06-FEB-2003.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.6e-11;
 RESULT 1160
 ID ABR65718 standard; protein; 649 AA.
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
 PN US2003036159-A1.
 PD 20-FEB-2003.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.6e-11;
 RESULT 1161
 ID ABU99658 standard; protein; 649 AA.
 DE Human secreted/transmembrane protein (PRO) #192.
 PN US2003040070-A1.
 PD 27-FEB-2003.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.6e-11;
 RESULT 1162
 ID ABUS2897 standard; protein; 649 AA.
 DE Human PRO polypeptide #192.
 PN US2003032113-A1.
 PD 13-FEB-2003.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.6e-11;
 RESULT 1163
 ID ABUS90018 standard; protein; 649 AA.
 DE Novel human secreted and transmembrane protein PRO1865.
 PN US2003036147-A1.
 PD 20-FEB-2003.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.6e-11;
 RESULT 1164
 ID ABR68267 standard; protein; 649 AA.
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
 PN US2003027264-A1.
 PD 06-FEB-2003.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.6e-11;
 RESULT 1165
 ID ABUS96320 standard; protein; 649 AA.
 DE Novel human secreted and transmembrane protein PRO1865.
 PN US2003036144-A1.
 PD 20-FEB-2003.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.6e-11;
 RESULT 1166
 ID ABUS92751 standard; protein; 649 AA.
 DE Human secreted/transmembrane protein (PRO) #192.
 PN US2003036149-A1.
 PD 20-FEB-2003.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.6e-11;
 RESULT 1167
 ID ABO08828 standard; protein; 649 AA.
 DE Human secreted/transmembrane protein (PRO) #192.
 PN US2003040062-A1.
 PD 06-MAR-2003.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.6e-11;
 RESULT 1168
 ID ABO02880 standard; protein; 649 AA.
 DE Human secreted/transmembrane protein (PRO) #192.
 PN US2003040062-A1.
 PD 27-FEB-2003.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.6e-11;
 RESULT 1169
 ID ABR75034 standard; protein; 649 AA.
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
 PN US2003040056-A1.

PD 27-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1170
ID ABR94796 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1171
ID ABU85769 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1172
ID ABUS9829 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003013153-A1
PD 16-JAN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1173
ID ABUS98144 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1174
ID ABUS91850 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1175
ID ABUS9543 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1176
ID ABUS6384 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1177
ID ABUS67597 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1178
ID ABUS0625 standard; protein; 649 AA.
DE Human PRO protein #192.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1179
ID ABUS0941 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.

PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1180
ID ABO34000 standard; protein; 649 AA.
DE Human secreted/transmembrane protein PRO1865.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1181
ID ABR99543 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1182
ID ABR98933 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1183
ID ABO16456 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1184
ID ABR92356 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1185
ID ABO18997 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1186
ID ABR78418 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1187
ID ABUS72017 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1188
ID ABUS5154 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1189
ID ABO00293 standard; protein; 649 AA.

DE Novel human secreted and transmembrane protein PRO1865.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1190 22.3%; Pred. No. 4.6e-11;
ID ABO11625 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1191 22.3%; Pred. No. 4.6e-11;
ID ABO02270 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1192 22.3%; Pred. No. 4.6e-11;
ID ABU88844 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1193 22.3%; Pred. No. 4.6e-11;
ID ABU83539 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1194 22.3%; Pred. No. 4.6e-11;
ID ABO06340 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1195 22.3%; Pred. No. 4.6e-11;
ID ABR59376 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1196 22.3%; Pred. No. 4.6e-11;
ID ABO09438 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1197 22.3%; Pred. No. 4.6e-11;
ID ABO19302 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1198 22.3%; Pred. No. 4.6e-11;
ID ABO11320 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1199 22.3%; Pred. No. 4.6e-11;
ID ABR66938 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003036148-A1.

PD 20-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1200 22.3%; Pred. No. 4.6e-11;
ID ABO16151 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1201 22.3%; Pred. No. 4.6e-11;
ID ABO13857 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1202 22.3%; Pred. No. 4.6e-11;
ID ABU71571 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1203 22.3%; Pred. No. 4.6e-11;
ID ABU65760 standard; protein; 649 AA.
DE Human secreted/transmembrane protein, SEQ ID 384.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1204 22.3%; Pred. No. 4.6e-11;
ID ABO07608 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1205 22.3%; Pred. No. 4.6e-11;
ID ABO03795 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1206 22.3%; Pred. No. 4.6e-11;
ID ABR67243 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1207 22.3%; Pred. No. 4.6e-11;
ID ABO15846 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1208 22.3%; Pred. No. 4.6e-11;
ID ABUS6127 standard; protein; 649 AA.
DE Human secreted/transmembrane protein, PRO1865.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1209 22.3%; Pred. No. 4.6e-11;
ID ABU72352 standard; protein; 649 AA.
DE Human PRO polypeptide #66.
PN US2002182638-A1.
PD 05-DEC-2002.

PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1210
ID ABU65455 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1211
ID ABU95400 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1212
ID ABU71303 standard; protein; 649 AA.
DE Human PRO1865 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1213
ID ABO07913 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1214
ID ABR70154 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1215
ID ABR69487 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1216
ID ABO01628 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1217
ID ABU81430 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1218
ID ABR0227 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1219
ID ABU91025 standard; protein; 649 AA.
DE Human PRO polypeptide #66.
PN US2003018168-A1.
PD 23-JAN-2003.

PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1220
ID ABR67962 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1221
ID ABR65350 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1222
ID ABR68572 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1223
ID ABR71984 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1224
ID ABU85464 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1225
ID ABU89154 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1226
ID ABU83234 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1227
ID ABU95090 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1228
ID ABU90638 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1229
ID ABU84149 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;

Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1230
ID ABU93800 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1231
ID ABR65045 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1232
ID ABR68877 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1233
ID ABO06693 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1234
ID ABR99238 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1235
ID ABU57122 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1236
ID ABU86074 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1237
ID ABU82361 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1238
ID ABU87372 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1239
ID ABU83644 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1240

ID ABO08218 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1241
ID ABU92541 standard; protein; 649 AA.
DE Human secreted/transmembrane protein PRO1865.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1242
ID ABU81929 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1243
ID ABU66093 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1244
ID ABU81211 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1245
ID ABR59922 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1246
ID ABU94110 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1247
ID ABU99963 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1248
ID ABR66633 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1249
ID ABR91051 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1250

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ID ABO53325 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1251
ID ABU94478 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1252
ID ABU79360 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1253
ID ABU86689 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1254
ID ABU86994 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1255
ID ABU94783 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1256
ID ABO04710 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1257
ID ABR70459 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1258
ID ABU98624 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1259
ID ABR66023 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1260
ID ABR64740 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003022293-A1.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1261
ID ABU79665 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1262
ID ABU93056 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1263
ID ABU96015 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1264
ID ABU91235 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1265
ID ABU90328 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1266
ID ABO09743 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1267
ID ABO11015 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1268
ID ABR71069 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1269
ID ABU98328 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1270
ID ABU87677 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003022293-A1.
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PD 30-JAN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1271
ID ABU91545 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1272
ID ABU89333 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1273
ID ABU84759 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1274
ID ABR69849 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1275
ID ABU80226 standard; protein; 649 AA.
DE Human PRO protein #192.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1276
ID ABU82540 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1277
ID ABU93495 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1278
ID ABO10048 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1279
ID ABO09133 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1280
ID ABU96504 standard; protein; 649 AA.
DE Human PRO polypeptide #66.
PN US2003027993-A1.
PD 06-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1281
ID ABU10701 standard; protein; 649 AA.
DE Human secreted/transmembrane protein #192.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1282
ID ABU72174 standard; protein; 649 AA.
DE Human PRO polypeptide #66.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1283
ID ABU95710 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1284
ID ABU96919 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1285
ID ABR70764 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1286
ID ABO05115 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1287
ID ABO08523 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1288
ID ABO05730 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1289
ID ABR74119 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1290
ID ABR95711 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.

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PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1291
ID ABR81008 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1292
ID ABR81313 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1293
ID ABR81009 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1294
ID ABR88611 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1295
ID ABR77432 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1296
ID ABO28916 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1297
ID ABO31661 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1298
ID ABO08078 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1299
ID ABO40558 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068682-A1.

PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1300
ID ABO35983 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1301
ID ABO44122 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1302
ID ADA78136 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1303
ID ABM24917 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003104539-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1304
ID ABO03185 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036131-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1305
ID ABR90441 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040075-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1306
ID ABM17355 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1307
ID ABR95101 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003044930-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1308
ID ABR95406 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1309
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PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1328
ID ABM21257 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1329
ID ABM09603 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1330
ID ABO41473 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1331
ID ABO36288 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1332
ID ABO33817 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1333
ID ABM76517 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003082717-A1.
PD 01-MAY-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1334
ID ABM76213 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1335
ID ABM25832 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003104542-A1.
PD 05-JUN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1336
ID ABM26137 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003104543-A1.
PD 05-JUN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1337
ID ABO33490 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036127-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1338
ID ABO02575 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1339
ID ABO44304 standard; protein; 649 AA.
DE Human secreted/transmembrane polypeptide PRO 1865.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1340
ID ABR90746 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1341
ID ABR73814 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1342
ID ABO17066 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1343
ID ABR94491 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1344
ID ABR75998 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003044929-A1.
PD 06-MAR-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1345
ID ABR71374 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1346
ID ABR93271 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
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Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. NO. 4.6e-11;
RESULT 1347
ID ABR93576 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. NO. 4.6e-11;
RESULT 1348
ID ABR88001 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. NO. 4.6e-11;
RESULT 1349
ID ABO28001 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
FN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. NO. 4.6e-11;
RESULT 1350
ID ABO30136 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
FN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. NO. 4.6e-11;
RESULT 1351
ID ABO33345 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
FN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. NO. 4.6e-11;
RESULT 1352
ID ABO50503 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. NO. 4.6e-11;
RESULT 1353
ID ABO808993 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. NO. 4.6e-11;
RESULT 1354
ID ABO36593 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
FN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. NO. 4.6e-11;
RESULT 1355
ID ABO35678 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
FN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. NO. 4.6e-11;

ID ABR87086 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1366
ID ABM1128 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1367
ID ABM28272 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1368
ID ABO32271 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1369
ID ABM15398 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1370
ID ABM06553 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1371
ID ABM04364 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1372
ID ABM22477 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1373
ID ABM07773 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1374
ID ABO40863 standard; protein; 649 AA.

DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1375
ID ABM35510 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1376
ID ABM33273 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1377
ID ABO52799 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1378
ID ABO50359 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1379
ID ABU99353 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1380
ID ABO04405 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036164-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1381
ID ABO06035 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003040074-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1382
ID ABM18575 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1383
ID ABR97603 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;

Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1403
ID ABO29221 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1404
ID ABM24002 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1405
ID ABM23392 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1406
ID ABM22172 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1407
ID ABO37813 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1408
ID ABM28577 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003082715-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1409
ID ABM28882 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003082716-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1410
ID ABM66526 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1411
ID ABM75908 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1412

ID ABM34188 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1413
ID ABM34493 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003100861-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1414
ID ABO20424 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003032125-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1415
ID ABO21339 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1416
ID ABO22254 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1417
ID ADA20166 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1418
ID ABR96688 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1419
ID ABR95866 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1420
ID ABR99848 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1421
ID ABM00399 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003073172-A1.

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PD 17-APR-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1422
ID ABM00704 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1423
ID ABO29831 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1424
ID ABM23697 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1425
ID ABM29492 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1426
ID ABO38423 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1427
ID ABO45723 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1428
ID ABM20647 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1429
ID ADA81655 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1430
ID ABO16761 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1431
ID ABO18387 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1432
ID ABO22814 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003027285-A1.
PD 06-FEB-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1433
ID ABO23119 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1434
ID ABR92661 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1435
ID ABR81618 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1436
ID ABM78042 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1437
ID ABR99831 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1438
ID ABM26747 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1439
ID ABM13873 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1440
ID ABO28611 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003064460-A1.
PD 03-APR-2003.
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PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1441
DE ABO30441 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1442
ID ABO30441 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1443
ID ABO30441 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1444
ID ABO37203 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1445
ID ABO41778 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1446
ID ABO35373 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1447
ID ABO25222 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1448
ID ABO47614 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1449
ID ABO47919 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1450
ID ABO48529 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1451
ID ABO51579 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1452
ID ABO51884 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1453
ID ABO50664 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1454
ID ABR79788 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1455
ID ABM17050 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1456
ID ABO18082 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1457
ID ABO21034 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1458
ID ABR96993 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1459
ID ABM12348 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
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PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1479
ID ABR76603 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1480
ID ABR73204 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1481
ID ABM18270 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1482
ID ABO20729 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1483
ID ABO25472 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1484
ID ABO25777 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1485
ID ABR94186 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1486
ID ABR80093 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1487
ID ABM11433 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1488
ID ABO33040 standard; protein; 649 AA.

DE Human PRO polypeptide #192.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1489
ID ABO30746 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1490
ID ABO31051 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1491
ID ABM27357 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1492
ID ABM30102 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1493
ID ABM05638 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1494
ID ABM15703 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1495
ID ABM08688 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1496
ID ABO42388 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1497
ID ABO38118 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.

PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1498
ID ABO46028 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1499
ID ARM66831 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1500
ID ADB20496 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003082767-A1.
PD 01-MAY-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;

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103	148.5	4.7	890	2	C95654	hypothetical prote	176	136	4.3	4957	2	T03455	ALR protein - huma
104	148.5	4.7	964	2	T49038	hypothetical prote	177	135.5	4.3	427	2	JC4915	ags protein precu
105	148.5	4.7	1115	2	S40241	G protein-coupled	178	135.5	4.3	499	2	D83333	hypothetical prote
106	148	4.7	338	2	S52284	lumicon, secretory	179	135.5	4.3	1124	2	B84742	probable receptor-
107	148	4.7	1188	2	S49915	extensin-like prot	180	135.5	4.3	5262	2	T03454	ALR protein - huma
108	147.5	4.7	316	2	A41781	proteoglycan-lb -	181	135	4.3	601	2	S56144	SH3 domain binding
109	147.5	4.7	1385	2	T13887	tlr protein - frui	182	134.5	4.3	613	2	T15489	hypothetical prote
110	147	4.7	1964	2	T90059	notch4 - mouse	183	134.5	4.3	847	2	F96531	hypothetical prote
111	147	4.7	2414	2	A54277	transcription adap	184	134.5	4.3	1039	2	T22117	hypothetical prote
112	146.5	4.7	382	2	T04260	hypothetical prote	185	134	4.3	530	2	A45690	transactivator EBN
113	146.5	4.7	925	2	C84538	probable LRR recep	186	134	4.3	656	2	B47096	hy1B homolog - Str
114	146.5	4.7	1408	2	S16148	gene serrate prote	187	134	4.3	886	2	T40734	probable adenylate
115	146	4.7	369	2	G83434	translocation prot	188	133.5	4.3	277	2	S25770	RSP-1 protein - mo
116	145.5	4.6	380	2	S71876	fibromodulin - chi	189	133.5	4.3	384	2	A41710	promastigote surfa
117	145.5	4.6	886	2	S23605	glycoprotein 350/2	190	133.5	4.3	1068	2	H96769	hypothetical prote
118	145.5	4.6	2142	2	B35098	MHC class III hist	191	133	4.2	576	2	T36729	probable serine/ch
119	145	4.6	458	2	T19941	hypothetical prote	192	133	4.2	852	2	I51259	tyrosine kinase C
120	145	4.6	679	2	T20713	hypothetical prote	193	133	4.2	932	2	T48489	receptor-like prot
121	145	4.6	694	2	JC2237	foliitropin recept	194	133	4.2	1257	2	A88536	protein B0523.5 [i
122	145	4.6	1839	1	OVBVK	adenylate cyclase	195	133	4.2	4391	2	A38096	perlecan precursor
123	144.5	4.6	486	2	B84460	hypothetical prote	196	132.5	4.2	463	1	A36479	milk fat globule m
124	144.5	4.6	2187	2	T30826	nascent polypeptid	197	132.5	4.2	2035	2	A40718	host cell factor C
125	144.5	4.6	3149	1	Q0BE8	BPLF1 protein - hu	198	132	4.2	3164	1	WMBEH6	UL36 protein - hum
126	144	4.6	695	2	I45896	follicle stimulat	199	131.5	4.2	346	2	T46916	hypothetical prote
127	144	4.6	1019	2	C96519	probable disease r	200	131.5	4.2	890	2	T00800	disease resistance
128	144	4.6	3020	2	A43932	mucin 2 precursor,	201	131.5	4.2	1097	2	A29943	Toll protein precu
129	143.5	4.6	243	2	B41710	promastigote surfa	202	131.5	4.2	1286	2	A88396	protein M0E10.2 [
130	143.5	4.6	476	2	T27051	hypothetical prote	203	131	4.2	612	2	T10727	protein kinase Xa2
131	143.5	4.6	496	2	C68832	hypothetical prote	204	131	4.2	767	2	B84594	probable LRR recep
132	143.5	4.6	605	2	T50817	protein serine/thr	205	131	4.2	905	2	T00475	probable disease r
133	143.5	4.6	683	2	T24486	hypothetical prote	206	131	4.2	915	2	T09575	smoothelin - human
134	142.5	4.5	1870	2	S37671	MHC class III hist	207	131	4.2	1095	2	C96746	hypothetical prote
135	142.5	4.5	1872	2	S36152	MHC class III hist	208	131	4.2	1196	2	T09356	brassinosteroid-in
136	142	4.5	661	2	I56258	RP105 - mouse	209	130.5	4.2	448	2	T27395	hypothetical prote
137	142	4.5	983	2	G84524	probable disease r	210	130	4.1	268	2	T19697	hypothetical prote
138	141.5	4.5	462	2	D84858	hypothetical prote	211	130	4.1	389	2	H86266	hypothetical prote
139	141.5	4.5	836	2	T46070	hypothetical prote	212	130	4.1	395	2	H75457	hypothetical prote
140	141.5	4.5	1029	2	T05050	protein kinase hom	213	130	4.1	768	2	T17462	disease resistance
141	141.5	4.5	1051	2	T13174	gp150 protein - fr	214	130	4.1	800	2	H84740	hypothetical prote
142	141	4.5	630	2	AC1129	internalin B [limp	215	129.5	4.1	315	2	T06806	proline rich prote
143	141	4.5	717	2	T33295	hypothetical prote	216	129.5	4.1	780	2	T00366	hypothetical prote
144	140.5	4.5	376	2	S55275	fibromodulin precu	217	129.5	4.1	861	2	A48825	Notch homolog Motc
145	140	4.5	277	2	I60122	rsu-1 homolog - hu	218	129.5	4.1	912	2	A54223	brevican precursor
146	140	4.5	474	2	S65763	chitinase (EC 3.2.	219	129.5	4.1	942	2	S23251	protein-tyrosine k
147	140	4.5	754	2	A85043	probable LRR recep	220	129.5	4.1	1173	2	I50620	proCK2 - chicken
148	140	4.5	1029	2	T00712	protein kinase hom	221	129.5	4.1	1469	2	T09219	basal transcriptio
149	139.5	4.4	333	2	T34555	hypothetical prote	222	129	4.1	371	2	S20075	promastigote surfa
150	139.5	4.4	527	2	A75399	hypothetical prote	223	129	4.1	835	2	T05259	probable disease r
151	139.5	4.4	539	2	G70520	probable csp prote	224	129	4.1	910	2	B96770	hypothetical prote
152	139.5	4.4	4351	2	T00252	MEGF1 protein - ra	225	129	4.1	1027	2	B85089	receptor protein k
153	139	4.4	581	2	A45551	insect-stage-speci	226	129	4.1	1064	2	B86465	probable Protein k
154	139	4.4	603	2	T24315	hypothetical prote	227	129	4.1	1232	2	T05322	hypothetical prote
155	139	4.4	720	2	T02361	hypothetical prote	228	129	4.1	1329	2	A64828	cell division prot
156	139	4.4	1088	2	E86312	FilA6.9 protein -	229	129	4.1	1342	2	B85614	cell division prot
157	139	4.4	2240	2	T37057	probable multi-dom	230	129	4.1	1342	2	G90750	cell division prot
158	138.5	4.4	342	2	A46743	lumican precursor	231	129	4.1	1959	1	AGRT	agrin - rat
159	138.5	4.4	990	2	T14756	hypothetical prote	232	129	4.1	2321	2	T78549	noctch3 protein - h
160	138.5	4.4	1650	2	S53457	dominant autoantig	233	128.5	4.1	477	2	S42442	nuclear protein BB
161	138	4.4	630	2	C39930	hypothetical prote	234	128.5	4.1	677	2	H86208	protein F22G5.26 [
162	138	4.4	858	2	T00258	hypothetical prote	235	128.5	4.1	727	2	C94534	hypothetical prote
163	138	4.4	1952	2	T48814	hypothetical prote	236	128.5	4.1	744	2	C94527	probable receptor-
164	137.5	4.4	1151	2	T18535	high molecular mas	237	128.5	4.1	825	2	T29634	hypothetical prote
165	137.5	4.4	4660	2	T42737	gp330 protein prec	238	128.5	4.1	1113	2	T00271	hypothetical prote
166	137	4.4	562	2	T34319	hypothetical prote	239	128.5	4.1	3968	2	A44265	trithorax homolog
167	137	4.4	695	2	JC1493	foliitropin recept	240	128	4.1	597	2	S72468	probable transcrip
168	137	4.4	788	2	AG0786	secreted effector	241	128	4.1	967	2	T48210	hypothetical prote
169	137	4.4	907	1	Q0BE21	membrane antigen g	242	128	4.1	1428	2	T08852	lustrin A - Califo
170	137	4.4	4544	1	S02392	alpha-2-macroglobu	243	128	4.1	1914	2	T42635	tenascin Y precurs
171	137	4.4	4545	1	S25111	alpha-2-macroglobu	244	127.5	4.1	750	2	D86245	hypothetical prote
172	136	4.3	322	2	S72271	proteoglycan lb pr	245	127.5	4.1	1120	2	B86479	hypothetical prote
173	136	4.3	626	2	AE0123	probable antigenic	246	127.5	4.1	1784	2	C96615	hypothetical prote
174	136	4.3	692	2	A34548	foliitropin recept	247	127	4.1	327	2	S20074	promastigote surfa
175	136	4.3	1008	2	D84434	probable receptor-	248	127	4.1	773	2	T00502	probable receptor-

249	127	4.1	775	1	EDBE11	immediate-early pr	322	121.5	3.9	432	2	E967112	unknown protein, 6
250	127	4.1	800	2	G84740	hypothetical prote	323	121.5	3.9	519	2	T07026	ethylene receptor
251	127	4.1	1366	2	T35985	probable large Pro	324	121.5	3.9	635	2	T07794	Delta-4 protein -
252	127	4.1	1895	2	T06609	disease resistance	325	121.5	3.9	686	2	JC7569	probable Pro kinase
253	127	4.1	1955	1	AGCH	agrin precursor -	326	121.5	3.9	760	2	F86387	hypothetical prote
254	126.5	4.0	288	2	T45616	hypothetical prote	327	121.5	3.9	902	2	T00588	latent transformin
255	126.5	4.0	685	2	JC7570	Delta-4 protein -	328	121.5	3.9	1251	2	A57293	presynaptic activi
256	126.5	4.0	694	2	JC4301	foliitropin recept	329	121.5	3.9	1409	2	T37188	fibronectin - bovi
257	126.5	4.0	862	2	T46289	hypothetical prote	330	121.5	3.9	2265	1	FNBO	polyketide synthas
258	126.5	4.0	999	1	S27756	receptor-like prot	331	121.5	3.9	2297	2	T34918	notch 3 protein -
259	126.5	4.0	1091	2	S33596	protein-tyrosine k	332	121.5	3.9	2318	2	S45306	unconventional myo
260	126.5	4.0	1777	2	T34369	hypothetical prote	333	121.5	3.9	3530	2	A59266	cell wall-plasma m
261	126	4.0	500	2	S49302	AWJ218 protein -	334	121	3.9	306	2	T52340	probable disease r
262	126	4.0	865	2	A47282	calcium-binding pr	335	121	3.9	480	2	T00971	sulfated surface g
263	126	4.0	873	2	A47283	calphotin - fruit	336	121	3.9	485	2	A33647	microtubule-associ
264	126	4.0	996	2	F86410	protein F3W18.12 (337	121	3.9	733	2	A45301	Notch B protein -
265	126	4.0	1152	2	T31911	hypothetical prote	338	121	3.9	1203	2	A49175	hypothetical prote
266	126	4.0	1820	2	A55494	latent transformin	339	121	3.9	1520	2	T00273	notch protein homo
267	125.5	4.0	283	2	S13383	hydroxyproline-ric	340	121	3.9	2531	2	S18188	osteoinductive fac
268	125.5	4.0	548	2	AH1107	internalin H (impo	341	120.5	3.8	299	2	A35272	Op protein - Kenne
269	125.5	4.0	635	2	F75477	hypothetical prote	342	120.5	3.8	753	2	JO0532	internalin, peptid
270	125.5	4.0	764	2	A40077	thyrotropin recept	343	120.5	3.8	821	2	AB1126	disease resistance
271	125.5	4.0	1003	2	T05898	hypothetical prote	344	120.5	3.8	855	2	T17460	probable receptor-
272	125	4.0	350	2	S22456	hydroxyproline-ric	345	120.5	3.8	976	2	B84659	protein kinase hom
273	125	4.0	476	2	A36478	surface glycoprote	346	120.5	3.8	976	2	T05897	receptor protein k
274	125	4.0	783	2	T45899	hypothetical prote	347	120.5	3.8	981	2	T50851	receptor protein k
275	125	4.0	818	2	F96586	hypothetical prote	348	120.5	3.8	987	2	T50850	mucin, tracheobron
276	125	4.0	991	2	T52400	receptor-like prot	349	120.5	3.8	1118	2	A48292	microtubule-associ
277	125	4.0	1504	2	T49896	glycine/proline-ri	350	120.5	3.8	1152	2	A33183	protein FilC7.4 (i
278	125	4.0	2026	1	OYBY	adenylate cyclase	351	120.5	3.8	1722	2	E99753	internalin protein
279	124.5	4.0	298	2	B35272	osteoinductive fac	352	120.5	3.8	1778	2	AF1116	tenascin-X precurs
280	124.5	4.0	756	2	T27642	hypothetical prote	353	120.5	3.8	3566	1	A40701	internalin protein
281	124.5	4.0	849	2	C97303	hypothetical prote	354	120	3.8	361	2	AH1469	probable cell wall
282	124.5	4.0	910	2	G84648	probable disease r	355	120	3.8	376	2	S71558	hypothetical prote
283	124.5	4.0	977	2	C96745	hypothetical prote	356	120	3.8	458	2	T31631	SH3 domains-contai
284	124.5	4.0	1223	2	E88451	protein K10D2.1 (i	357	120	3.8	892	2	T09071	receptor-like prot
285	124.5	4.0	2176	2	T13806	toucan gene protei	358	120	3.8	962	2	T04124	hypothetical prote
286	124	4.0	496	2	D75261	conserved hypotet	359	120	3.8	1126	2	T20801	webi protein homol
287	124	4.0	543	2	S35047	mucin JUL7 - human	360	120	3.8	1224	2	T40765	cell wall glycopro
288	124	4.0	574	2	T43556	Wiskott-Aldrich sy	361	119.5	3.8	267	2	S08314	transcription fact
289	124	4.0	605	2	AG0123	probable antigenic	362	119.5	3.8	479	1	A31753	receptor protein k
290	124	4.0	729	2	E70803	hypothetical prote	363	119.5	3.8	660	2	T45569	large structural p
291	124	4.0	766	2	B85440	receptor kinase-li	364	119.5	3.8	1048	1	XPBEA9	probable receptor
292	124	4.0	978	2	E96787	protein T4012.5 (i	365	119.5	3.8	1079	2	C96772	protein F20N2.4 (i
293	124	4.0	1011	2	T45718	receptor-kinase li	366	119.5	3.8	1166	2	F96598	hypothetical prote
294	124	4.0	1472	2	B54774	ATP binding cassat	367	119.5	3.8	1400	2	B70963	hypothetical prote
295	124	4.0	4135	2	T42629	tenascin-X - bovin	368	119.5	3.8	1596	2	A35927	190K DNA-binding p
296	123.5	3.9	380	2	T01281	probable leucine-r	369	119.5	3.8	1643	2	T14274	versican precursor
297	123.5	3.9	492	2	F86263	hypothetical prote	370	119	3.8	164	2	I53641	mucin SAC - human
298	123.5	3.9	656	2	AE1479	probable cell surf	371	119	3.8	352	2	S49299	AWJ1172 protein -
299	123.5	3.9	690	2	T41296	hypothetical prote	372	119	3.8	424	2	S27783	hypothetical prote
300	123	3.9	528	2	T15198	probable alcohol d	373	119	3.8	550	2	C75557	hypothetical prote
301	123	3.9	574	2	T38819	wiskott-aldrich sy	374	119	3.8	651	2	T42644	BHLFI protein - hu
302	123	3.9	888	2	S23065	ufo protein - mous	375	119	3.8	660	1	Q0BE3	hypothetical prote
303	123	3.9	1072	2	A37127	microtubule-associ	376	119	3.8	808	2	T23129	hypothetical prote
304	123	3.9	2591	2	T30288	priestnamycin I sy	377	119	3.8	864	2	D84740	hypothetical prote
305	122.5	3.9	303	2	S28264	hydroxyproline-ric	378	119	3.8	1006	2	T42731	atrophin-1 related
306	122.5	3.9	415	2	T13435	hypothetical prote	379	119	3.8	1045	2	T41119	internalin - relate
307	122.5	3.9	592	2	D70863	hypothetical prote	380	118.5	3.8	222	2	H96711	hypothetical prote
308	122.5	3.9	699	2	T05225	extensin homolog F	381	118.5	3.8	400	1	A39822	leukostialin precu
309	122.5	3.9	809	2	B84634	probable receptor-	382	118.5	3.8	677	2	E70722	hypothetical prote
310	122.5	3.9	845	2	T12537	hypothetical prote	383	118.5	3.8	751	2	AC2098	hypothetical prote
311	122.5	3.9	1016	2	T30553	disease resistance	384	118.5	3.8	869	2	A71400	probable disease r
312	122.5	3.9	2944	2	A54849	collagen alpha 1(V	385	118.5	3.8	883	2	S57653	prevican precursor
313	122	3.9	298	2	JC4130	osteoglycin precu	386	118.5	3.8	988	2	T45717	receptor-kinase li
314	122	3.9	326	2	T42732	hypothetical prote	387	118.5	3.8	1173	2	T25893	hypothetical prote
315	122	3.9	596	2	AE1515	internalin like pr	388	118.5	3.8	1356	2	A45445	janusin precursor,
316	122	3.9	623	2	T19876	hypothetical prote	389	118.5	3.8	1607	2	T02837	long chain fatty a
317	122	3.9	672	2	B84782	probable receptor-	390	118	3.8	294	2	A37232	mucin, tracheal (A
318	122	3.9	715	2	G86239	protein F20B24.6 (391	118	3.8	599	2	T10798	phosphorin-S - Vo
319	122	3.9	719	2	T47727	hypothetical prote	392	118	3.8	667	2	S74254	homeotic protein s
320	122	3.9	921	2	B86234	hypothetical prote	393	118	3.8	823	2	AD1935	general secretion
321	122	3.9	992	2	T05335	hypothetical prote	394	118	3.8	1134	1	JD0711	protein-tyrosine k

395	118	3.8	2471	2	A49128	cell-fate determin	468	114	3.6	378	2	S00842	leukosialin precu
396	117.5	3.7	473	2	D85041	hypothetical prote	469	114	3.6	413	1	A34888	transcription fact
397	117.5	3.7	624	2	A55576	collagen alpha 2(X	470	114	3.6	555	1	S20100	mullerian inhibiti
398	117.5	3.7	660	2	JW0067	chitinase (EC 3.2.	471	114	3.6	586	2	T29695	hypothetical prote
399	117.5	3.7	996	2	T10725	protein kinase Xa2	472	114	3.6	633	2	S62057	proline-rich prote
400	117.5	3.7	1075	2	D70568	hypothetical prote	473	114	3.6	634	2	T00388	hypothetical prote
401	117.5	3.7	1706	2	I84499	zinc finger protei	474	114	3.6	656	2	E75468	hypothetical prote
402	117	3.7	431	2	T27904	hypothetical prote	475	114	3.6	768	2	A42755	P-selectin precurs
403	117	3.7	655	1	A46688	hepatocyte growth	476	114	3.6	1290	2	T00018	period protein hom
404	117	3.7	670	2	J96707	probable receptor	477	114	3.6	2225	2	T26063	hypothetical prote
405	117	3.7	678	2	JC4245	transcription fact	478	113.5	3.6	317	2	S55316	mucin (clone PGM-2
406	117	3.7	743	2	C84633	probable disease r	479	113.5	3.6	330	2	T46256	brevican - human (
407	117	3.7	801	2	T29018	hypothetical prote	480	113.5	3.6	538	2	T01102	disease resistance
408	117	3.7	1007	2	C84668	probable receptor-	481	113.5	3.6	896	2	B43817	transforming prote
409	117	3.7	1009	2	D75399	probable penicilli	482	113.5	3.6	907	2	A86460	99.9K hypothetical
410	117	3.7	1328	2	T43060	agrin - electric r	483	113.5	3.6	938	1	Q08E24	nuclear antigen EB
411	117	3.7	1450	2	T30273	hypothetical prote	484	113.5	3.6	1286	2	T33476	hypothetical prote
412	117	3.7	1574	2	T13954	MEGF6 protein - ra	485	113.5	3.6	1907	2	S50893	protein-tyrosine-p
413	117	3.7	2082	2	T37056	probable multi-dom	486	113.5	3.6	2911	2	T20566	hypothetical prote
414	117	3.7	2332	2	T34434	hypothetical prote	487	113	3.6	371	2	T49908	hypothetical prote
415	116.5	3.7	279	2	S53363	mucin SAC (clone J	488	113	3.6	377	2	A48018	mucin 7 precursor,
416	116.5	3.7	439	2	S51939	chitinase (EC 3.2.	489	113	3.6	382	2	E84527	hypothetical prote
417	116.5	3.7	621	2	I38467	low density lipopr	490	113	3.6	419	2	A90888	hypothetical prote
418	116.5	3.7	787	2	T27632	hypothetical prote	491	113	3.6	419	2	H85729	hypothetical prote
419	116.5	3.7	794	2	T27633	hypothetical prote	492	113	3.6	603	2	A75373	probable N-acetyl
420	116.5	3.7	828	2	A88860	protein ZC518.3 [i	493	113	3.6	979	2	A35913	regulatory factor
421	116.5	3.7	1048	2	T31425	C-terminal domain-	494	113	3.6	982	2	A53253	microtubule-associ
422	116.5	3.7	1446	1	A45344	immediate-early pr	495	113	3.6	1002	2	T46033	receptor protein k
423	116.5	3.7	2229	2	T16199	hypothetical prote	496	113	3.6	1025	2	T45647	receptor protein k
424	116	3.7	292	2	S24169	mucin - rat	497	113	3.6	1069	2	S27922	nuclear antigen EB
425	116	3.7	652	2	S71753	repellent protein	498	113	3.6	1247	2	T42209	neural plakophilin
426	116	3.7	660	2	AH2348	hypothetical prote	499	113	3.6	1343	2	T42209	cell division prot
427	116	3.7	729	2	F86308	Similar to disease	500	113	3.6	1343	2	A70611	alpha-A-crystallin
428	116	3.7	771	2	T02565	disease resistance	501	113	3.6	3381	2	T42389	versican precursor
429	116	3.7	808	2	B97303	hypothetical prote	502	112.5	3.6	347	2	S10571	mucin 1 precursor,
430	116	3.7	845	2	T07039	Hcr-9-0 protein - t	503	112.5	3.6	581	2	G96811	unknown protein T1
431	116	3.7	907	2	A24938	hypothetical T2 pr	504	112.5	3.6	731	2	B86369	hypothetical prote
432	116	3.7	1291	2	T00019	period protein hom	505	112.5	3.6	1075	2	A57377	transcription fact
433	116	3.7	1494	2	T13255	protein-tyrosine-p	506	112.5	3.6	1237	2	AC1583	internalin protein
434	116	3.7	1840	2	T30250	Grl protein - mous	507	112.5	3.6	1680	2	T01367	hypothetical prote
435	116	3.7	2531	2	A46019	notch-1 protein -	508	112.5	3.6	2479	2	F87386	conserved hypotet
436	116	3.7	2555	2	A40043	notch protein homo	509	112.5	3.6	4006	2	T09070	probable tenascin
437	116	3.7	2774	2	A43359	microtubule-associ	510	112	3.6	241	2	S32359	glial growth facto
438	115.5	3.7	322	2	A53715	apomucin precursor	511	112	3.6	252	2	T01787	thyrotropin recept
439	115.5	3.7	513	2	AC3061	hypothetical prote	512	112	3.6	253	1	JC1319	thyrotropin recept
440	115.5	3.7	513	2	D98225	hypothetical prote	513	112	3.6	285	2	A41826	probable pheromone
441	115.5	3.7	528	2	I47141	gastric mucin (clo	514	112	3.6	383	2	S53716	delta-like homeoti
442	115.5	3.7	696	2	T42659	hypothetical prote	515	112	3.6	413	2	S48756	transcription fact
443	115.5	3.7	805	2	T49385	hypothetical prote	516	112	3.6	704	2	A52107	serine/threonine k
444	115.5	3.7	946	2	S27921	nuclear antigen EB	517	112	3.6	731	2	T04455	hypothetical prote
445	115.5	3.7	1093	2	I38533	AFI7 protein - hum	518	112	3.6	742	2	F84643	hypothetical prote
446	115.5	3.7	1268	2	S52781	neurocan - mouse	519	112	3.6	764	1	QRHURH	thyrotropin recept
447	115.5	3.7	1460	1	EDBEIF	immediate-early pr	520	112	3.6	883	2	S49126	brevican precursor
448	115.5	3.7	2214	2	T16305	hypothetical prote	521	112	3.6	960	2	G84652	probable receptor-
449	115.5	3.7	3421	1	WZBBE6	367K tegument prot	522	112	3.6	990	2	T03784	probable receptor
450	115	3.7	404	2	T08549	hypothetical prote	523	112	3.6	1032	2	T34433	hypothetical prote
451	115	3.7	451	2	S74728	hypothetical prote	524	112	3.6	1289	2	AE2217	hypothetical prote
452	115	3.7	461	1	T10741	extensin-like prot	525	111.5	3.6	224	2	D72861	Gene BCRF2 protein
453	115	3.7	479	1	S22542	transcription fact	526	111.5	3.6	383	2	S32975	AcOrf-91 protein -
454	115	3.7	539	2	AH2116	internalin, probab	527	111.5	3.6	478	1	I47154	transcription fact
455	115	3.7	766	2	T01817	hypothetical prote	528	111.5	3.6	645	2	T05251	probable disease r
456	115	3.7	838	2	T08423	Axin homolog Axll	529	111.5	3.6	649	2	T46500	hypothetical prote
457	115	3.7	980	2	T05414	protein kinase hom	530	111.5	3.6	1047	2	A55617	masquerade precurs
458	115	3.7	1133	2	E86308	hypothetical prote	531	111.5	3.6	1253	2	T45787	disease resistance
459	115	3.7	1220	1	A56136	jagged protein pre	532	111.5	3.6	1298	1	EDBE75	immediate-early pr
460	115	3.7	2415	1	A39086	aggrekan precursor	533	111.5	3.6	1353	1	JH0675	restrictin precurs
461	114.5	3.7	328	2	JQ0985	hydroxyproline-ric	534	111.5	3.6	2649	2	T51023	hypothetical prote
462	114.5	3.7	409	2	T11743	pp47 protein - pig	535	111	3.6	274	2	JC8083	heart-restricted l
463	114.5	3.7	505	2	AC1469	internalin like pr	536	111	3.5	478	2	H86459	hypothetical prote
464	114.5	3.7	606	2	T51880	hypothetical prote	537	111	3.5	509	2	T05260	probable disease r
465	114.5	3.7	627	2	T27123	hypothetical prote	538	111	3.5	518	2	S50465	PAC2 protein - yea
466	114.5	3.7	638	2	T05606	protein kinase hom	539	111	3.5	548	2	E70546	hypothetical prote
467	114	3.6	218	2	T01104	disease resistance	540	111	3.5	603	2	S28941	coagulation factor

687	107	3.4	1389	2	I58157	periaxin - rat	760	105	3.3	1133	2	A54164	sterol regulatory
688	107	3.4	2723	2	T03221	probable polyketid	761	105	3.3	1135	2	T30561	scythe protein - A
689	107	3.4	7463	2	T36248	CDA peptide synthe	762	105	3.3	1136	1	S57845	protein-tyrosine k
690	106.5	3.4	3024	2	A32993	transcription fact	763	105	3.3	1456	2	T01397	LTR gag/pol polypr
691	106.5	3.4	353	2	A41558	N-syndecin - rat (764	105	3.3	1658	2	D75489	hypothetical prote
692	106.5	3.4	505	2	B46629	mucin 6, gastric (765	105	3.3	1844	2	S01956	hypothetical prote
693	106.5	3.4	509	2	D86911	conserved hypotet	766	105	3.3	2133	2	T30637	hypothetical prote
694	106.5	3.4	509	2	T10013	probable phosphor	767	105	3.3	2409	1	A60979	vesican precursor
695	106.5	3.4	517	2	AD1570	interleukin, probab	768	105	3.3	2769	1	UIBO	thyroglobulin prec
696	106.5	3.4	620	2	S06733	hydroxyproline-ric	769	104.5	3.3	329	2	T17033	hypothetical prote
697	106.5	3.4	827	2	AC2963	cellB protein [limp	770	104.5	3.3	407	2	C70816	hypothetical prote
698	106.5	3.4	925	2	H96638	protein Tlf9-20 [i	771	104.5	3.3	464	2	T35943	probable hydrolyti
699	106.5	3.4	988	2	C75489	conserved hypotet	772	104.5	3.3	530	2	T32812	hypothetical prote
700	106.5	3.4	1003	2	T13856	ksr protein - frui	773	104.5	3.3	639	2	G02919	transcription fact
701	106.5	3.4	1161	2	S57180	probable membrane	774	104.5	3.3	662	2	T04856	hypothetical prote
702	106.5	3.4	1184	2	S05832	atrophin-1 - human	775	104.5	3.3	700	2	A42395	lutropin receptor
703	106.5	3.4	1305	2	AB0168	probable cell divi	776	104.5	3.3	707	1	A34458	gelatinase B (EC 3
704	106.5	3.4	1442	2	T42607	transcription acti	777	104.5	3.3	707	1	A53796	gelatinase B (EC 3
705	106.5	3.4	1892	2	T18314	hypothetical prote	778	104.5	3.3	744	2	T35192	probable ABC trans
706	106.5	3.4	2090	2	S26058	probable transform	779	104.5	3.3	755	2	T20950	hypothetical prote
707	106.5	3.4	2453	2	S02254	nuclear receptor c	780	104.5	3.3	909	1	QRXLL1	LDL receptor 1 pre
708	106	3.4	135	2	T49996	AtAGP4 - Arabidops	781	104.5	3.3	960	1	S28262	kinesin-related pr
709	106	3.4	167	2	A33532	mucin SMUC-40 - hu	782	104.5	3.3	1117	2	JC4934	delta-crystallin/E
710	106	3.4	216	2	I51920	mucin - rhesus mac	783	104.5	3.3	1194	2	E96624	hypothetical prote
711	106	3.4	287	2	S65765	chitinase (EC 3.2.	784	104.5	3.3	1241	2	T37190	nephthrin - human
712	106	3.4	405	2	S78691	flagellar hook-len	785	104.5	3.3	1505	2	JC4851	hypoxia-inducible
713	106	3.4	431	2	S47538	acrosin (EC 3.4.21	786	104.5	3.3	1851	2	T19964	hypothetical prote
714	106	3.4	435	2	D41602	transcription fact	787	104.5	3.3	1898	2	S46216	leukocyte antigen-
715	106	3.4	443	2	B39794	transcription fact	788	104.5	3.3	2117	2	T36180	CDA peptide synthe
716	106	3.4	449	2	A24993	cellulase (EC 3.2.	789	104	3.3	232	2	A60095	larval glue protei
717	106	3.4	567	2	A45977	Rab geranylgeranyl	790	104	3.3	306	2	I49139	lymphotoxin-beta -
718	106	3.4	666	2	B70803	hypothetical prote	791	104	3.3	318	2	B64900	hypothetical prote
719	106	3.4	701	2	D48613	gag polyprotein -	792	104	3.3	326	2	A46676	CD68 homolog macro
720	106	3.4	812	2	T01105	disease resistance	793	104	3.3	332	2	S43988	protein phosphatas
721	106	3.4	828	2	T51049	related to nucleol	794	104	3.3	360	2	S68209	sds22 protein homo
722	106	3.4	850	2	S56015	gastric mucin MUC5	795	104	3.3	365	2	A39481	serum response fac
723	106	3.4	901	2	A49227	sialidase - Actino	796	104	3.3	426	2	D88103	protein W10G11.6 [
724	106	3.4	914	2	T17233	hypothetical prote	797	104	3.3	440	2	I49681	glyceraldehyde-3-p
725	106	3.4	1064	2	A40136	fibropellin Ia - s	798	104	3.3	440	2	S36536	L2 protein - human
726	106	3.4	1603	2	A48613	gag/pol polyprotei	799	104	3.3	537	2	A46611	myosin-binding pro
727	106	3.4	1958	2	B40505	hypothetical prote	800	104	3.3	538	2	S65764	chitinase (EC 3.2.
728	106	3.4	2554	1	TVPF7L	kinase-related pro	801	104	3.3	593	2	S49525	glycoprotein G - s
729	106	3.4	3938	2	T42761	Bassoon protein	802	104	3.3	712	1	I46031	gelatinase B (EC 3
730	105.5	3.4	395	2	T01392	leucine-rich repea	803	104	3.3	895	2	S20582	dyscrophin-associ
731	105.5	3.4	486	2	A41537	DNA-binding protei	804	104	3.3	927	2	T24031	hypothetical prote
732	105.5	3.4	510	2	A42750	insulinoma-associ	805	104	3.3	1045	2	T16275	hypothetical prote
733	105.5	3.4	668	2	T05257	probable disease r	806	104	3.3	1547	2	T28657	blackjack protein,
734	105.5	3.4	688	2	T04568	protein kinase hom	807	104	3.3	1575	2	S68448	synaptojanin, 170K
735	105.5	3.4	695	2	S62400	amphiphysin (clone	808	104	3.3	1711	2	T31337	1,4-beta-glucanase
736	105.5	3.4	772	2	T13078	KiAA0992 protein -	809	104	3.3	1744	2	A54970	tensin, cardiac mu
737	105.5	3.4	780	2	A48143	HF-1 regulatory el	810	104	3.3	3507	2	T34513	hypothetical prote
738	105.5	3.4	952	2	S32954	hypothetical prote	811	103.5	3.3	206	1	NBHUIB	platelet glycoprot
739	105.5	3.4	1132	2	A30065	MHC class III hist	812	103.5	3.3	261	2	P00478	pistil extensin-li
740	105.5	3.4	1172	2	T00065	hypothetical prote	813	103.5	3.3	284	2	D70845	hypothetical prote
741	105.5	3.4	1521	2	T15264	hypothetical prote	814	103.5	3.3	393	2	P00479	pistil extensin-li
742	105.5	3.4	1712	2	A38261	masking protein pr	815	103.5	3.3	411	1	I55604	platelet glycoprot
743	105.5	3.4	1839	1	RRWPEM	genome polyprotein	816	103.5	3.3	419	2	T49292	hypothetical prote
744	105.5	3.4	2477	2	S14428	fibronectin precu	817	103.5	3.3	444	1	A39794	transcription fact
745	105.5	3.4	3033	1	JQ1303	genome polyprotein	818	103.5	3.3	489	2	F75591	p49 secreted prote
746	105	3.3	349	2	T05857	hypothetical prote	819	103.5	3.3	625	2	A26456	nicotinic acetylch
747	105	3.3	422	2	I37891	interleukin-1l rec	820	103.5	3.3	654	2	T33044	hypothetical prote
748	105	3.3	454	2	E75291	probable cell wall	821	103.5	3.3	889	2	F96637	hypothetical prote
749	105	3.3	460	2	T33110	hypothetical prote	822	103.5	3.3	898	2	T20123	hypothetical prote
750	105	3.3	486	1	A57601	transcription fact	823	103.5	3.3	968	2	T00353	hypothetical prote
751	105	3.3	511	1	VGBEF4	glycoprotein C - h	824	103.5	3.3	975	2	I48974	receptor-protein t
752	105	3.3	566	2	T34842	probable transfer	825	103.5	3.3	980	2	S54986	regulatory protein
753	105	3.3	620	2	T05125	hypothetical prote	826	103.5	3.3	1020	2	A29355	fibronectin - chic
754	105	3.3	658	2	T08153	cysteine proteinas	827	103.5	3.3	1144	2	A54810	TMV resistance pro
755	105	3.3	730	2	JC1456	gelatinase B (EC 3	828	103.5	3.3	1171	2	T35548	hypothetical prote
756	105	3.3	764	2	JC5643	thyroid stimulat	829	103.5	3.3	1268	2	T31420	C-terminal domain-
757	105	3.3	847	1	A53800	mixed-lineage prot	830	103.5	3.3	1590	2	B86398	protein T7N9.24 [i
758	105	3.3	895	2	I54343	dysroglycan - hum	831	103.5	3.3	1603	2	S23810	collagen alpha 1(X
759	105	3.3	976	2	A36355	protein-tyrosine k	832	103.5	3.3	1638	2	A42091	transcription acti

833	103.5	3.3	1733	1	B45344	probable nuclear a	906	102	3.3	567	2	JC5538	Rab geranylgeranyl
834	103.5	3.3	3739	2	T17410	polyketide synthas	907	102	3.3	585	1	B70747	probable serine/th
835	103	3.3	168	2	S52994	arabinogalactan-li	908	102	3.3	650	2	B87791	protein B0207.1 li
836	103	3.3	291	2	E84740	hypothetical prote	909	102	3.3	670	2	S22293	zinc finger protei
837	103	3.3	227	2	T27905	hypothetical prote	910	102	3.3	715	2	T12534	hypothetical prote
838	103	3.3	263	2	S01360	salivary glue prot	911	102	3.3	722	2	I48324	DELTA-like 1 - mou
839	103	3.3	362	2	A44083	meq protein - Mare	912	102	3.3	728	2	D86278	hypothetical prote
840	103	3.3	367	2	AC1328	internalin protein	913	102	3.3	890	2	E84846	probable receptor-
841	103	3.3	379	2	T16213	APX-1 protein homo	914	102	3.3	896	1	A35782	cytokine receptor
842	103	3.3	394	2	C84905	probable extensin	915	102	3.3	923	2	A35956	progesterone recep
843	103	3.3	515	2	F70904	hypothetical prote	916	102	3.3	963	2	A55926	DNA binding protei
844	103	3.3	535	1	S76953	protein kinase (EC	917	102	3.3	1008	2	T04462	hypothetical prote
845	103	3.3	550	2	G70597	probable proteinas	918	102	3.3	1021	2	H75423	hypothetical prote
846	103	3.3	575	2	JG0181	Xill2 protein - hu	919	102	3.3	1032	2	D83637	serine/threonine p
847	103	3.3	611	2	B86387	unknown protein [i	920	102	3.3	1052	2	B49120	protein-tyrosine k
848	103	3.3	648	2	T35120	hypothetical prote	921	102	3.3	1069	2	D85383	hypothetical prote
849	103	3.3	701	2	F48613	gag polyprotein -	922	102	3.3	1137	2	A86335	T20H2.9 protein -
850	103	3.3	793	2	JC7390	thyroid stimulat	923	102	3.3	1166	2	T13958	synGAP-b1 protein
851	103	3.3	799	1	TVR1TB	nerve growth facto	924	102	3.3	1249	2	T14270	Ras-GTPase activat
852	103	3.3	813	2	T04313	protein kinase Xa2	925	102	3.3	1293	2	T14259	Ras-GTPase activat
853	103	3.3	851	2	S67285	NUD1 protein - yea	926	102	3.3	1692	2	A33988	adenylate cyclase
854	103	3.3	863	2	A55173	cf-9 protein precu	927	102	3.3	1985	2	S19151	hypothetical prote
855	103	3.3	915	2	S36327	clathrin assembly	928	102	3.3	2218	2	B84683	hypothetical prote
856	103	3.3	1040	2	T23092	TSC-22 protein hom	929	102	3.3	2437	2	S42612	transmembrane prot
857	103	3.3	1121	2	A82809	exodeoxyribonuclea	930	102	3.3	2440	2	S39161	transcription coac
858	103	3.3	1199	2	A40670	nuclear envelope p	931	102	3.3	2441	2	S39161	CRBP-binding prote
859	103	3.3	1201	2	G86441	unknown protein [i	932	102	3.3	3124	2	A40020	collagen alpha 1(X
860	103	3.3	1275	2	T33369	hypothetical prote	933	102	3.3	5147	1	LJFFTM	cadherin-related t
861	103	3.3	1340	2	A39808	proteoglycan core	934	101.5	3.2	98	2	S53367	mucin SAC (clone M
862	103	3.3	1541	2	T02831	AAA protein L4171.	935	101.5	3.2	173	2	T47176	hypothetical prote
863	103	3.3	1894	2	C54689	protein-tyrosine-p	936	101.5	3.2	242	2	A40428	nonspecific cross-
864	103	3.3	2207	1	GNNY5P	genome polyprotein	937	101.5	3.2	372	2	T29359	hypothetical prote
865	103	3.3	2481	2	A43908	fibronectin - Afri	938	101.5	3.2	409	2	T43599	YOP targeted effec
866	103	3.3	3133	2	S52093	hemocytin - silkw	939	101.5	3.2	547	2	B56573	nuclear pore compl
867	102.5	3.3	217	2	S01358	salivary glue prot	940	101.5	3.2	654	2	C87587	hypothetical prote
868	102.5	3.3	252	2	T04739	hypothetical prote	941	101.5	3.2	657	2	B84869	probable Sfr16 prot
869	102.5	3.3	316	2	T31880	hypothetical prote	942	101.5	3.2	710	2	T44753	hypothetical prote
870	102.5	3.3	338	2	IS3043	transforming prote	943	101.5	3.2	728	2	IS0719	C-Delta-1 - chicke
871	102.5	3.3	352	2	S17313	transcription fact	944	101.5	3.2	733	2	A87168	conserved hypotet
872	102.5	3.3	371	2	F70555	hypothetical prote	945	101.5	3.2	833	2	A22089	hypothetical prote
873	102.5	3.3	379	2	S31719	proline-rich prote	946	101.5	3.2	869	2	A53384	transcription fact
874	102.5	3.3	383	2	B86272	protein Fl6A14.12	947	101.5	3.2	921	2	S40495	collagen alpha 1(I
875	102.5	3.3	385	2	S53718	homeotic protein d	948	101.5	3.2	947	2	G86420	probable receptor-
876	102.5	3.3	385	2	A54785	preadipocyte facto	949	101.5	3.2	972	2	IS2657	seizure-related pr
877	102.5	3.3	421	2	T30709	core protein homol	950	101.5	3.2	984	1	A34076	protein-tyrosine k
878	102.5	3.3	507	1	A32385	erythropoietin rec	951	101.5	3.2	1034	2	JC5569	serine proteinase
879	102.5	3.3	627	2	D75393	serine proteinase,	952	101.5	3.2	1039	2	A85096	hypothetical prote
880	102.5	3.3	674	2	T05264	probable serine/th	953	101.5	3.2	1429	2	S06434	homeotic protein l
881	102.5	3.3	706	2	E30411	synapsin Ia - bovi	954	101.5	3.2	1668	2	T13748	sex comb protein -
882	102.5	3.3	730	1	IS2580	gelatinase B (EC 3	955	101.5	3.2	1733	2	S27939	tensin - chicken
883	102.5	3.3	760	1	S07896	transcription fact	956	101.5	3.2	4543	1	A53102	alpha-2-macroglobu
884	102.5	3.3	904	2	T46170	disease resistance	957	101	3.2	240	2	B24264	proline-rich prote
885	102.5	3.3	907	2	E96636	hypothetical prote	958	101	3.2	249	2	S72619	hypothetical prote
886	102.5	3.3	942	1	QJ1674	protein kinase TMK	959	101	3.2	294	2	T34537	hypothetical prote
887	102.5	3.3	964	2	JC5545	integrin beta-4 pr	960	101	3.2	360	2	S25561	transcription fact
888	102.5	3.3	1013	2	T46422	hypothetical prote	961	101	3.2	373	2	A44478	probable cell grow
889	102.5	3.3	1115	1	IJWSNL	neural cell adhesi	962	101	3.2	401	2	A48423	engrailed homeodom
890	102.5	3.3	1223	2	T15316	hypothetical prote	963	101	3.2	482	2	A44997	merozoite surface
891	102.5	3.3	1350	2	G36793	hypothetical prote	964	101	3.2	492	2	B86911	probable penicilli
892	102.5	3.3	1367	1	S48478	glucan 1,4-alpha-g	965	101	3.2	574	2	B87619	sensor histidine k
893	102.5	3.3	1678	2	T35547	hypothetical prote	966	101	3.2	610	2	A28798	myosin-light-chain
894	102.5	3.3	1779	2	T31085	xylanase - Caldice	967	101	3.2	613	2	A40497	dihydrolipoamide S
895	102.5	3.3	1813	2	T30564	resistance protein	968	101	3.2	615	1	XXHU	dihydrolipoamide S
896	102.5	3.3	1863	2	S46217	protein-tyrosine-p	969	101	3.2	628	2	JQ0110	hypothetical 69K p
897	102.5	3.3	1875	2	A36429	integrin beta-4 ch	970	101	3.2	671	2	D84648	probable disease r
898	102.5	3.3	2207	2	S09553	genome polyprotein	971	101	3.2	688	2	T18263	S-layer protein -
899	102	3.3	301	2	JQ1663	hybrid proline-ric	972	101	3.2	700	2	D70951	probable UvrD - My
900	102	3.3	307	2	S36779	ribosome-binding p	973	101	3.2	739	2	IS6187	transcription fact
901	102	3.3	317	2	A28996	proline-rich prote	974	101	3.2	796	2	T21460	hypothetical prote
902	102	3.3	353	2	B38963	bcsA 5'-region pro	975	101	3.2	846	1	Q8BEC3	HQRF1 protein - hu
903	102	3.3	413	2	T49545	hypothetical prote	976	101	3.2	1043	2	A56037	DNA-binding protei
904	102	3.3	532	2	S74453	hypothetical prote	977	101	3.2	1127	2	T32404	hypothetical prote
905	102	3.3	554	1	FQHUMP	macrophage colony-	978	101	3.2	1257	2	S28764	neurocan precursor

979 101 3.2 1367 2 T33819 hypothetical prote
980 101 3.2 1513 2 A54895 mucin 2, intestina
981 101 3.2 1792 2 A57075 tensin - chicken (
982 101 3.2 2946 2 T15840 hypothetical prote
983 101 3.2 3176 2 CGHU3A collagen alpha 3(V
984 100.5 3.2 1378 2 D96715 protein F4N2.10 [i
985 100.5 3.2 1368 2 T33408 hypothetical prote
986 100.5 3.2 262 2 E88400 protein H34124.2 [i
987 100.5 3.2 269 2 T28957 hypothetical prote
988 100.5 3.2 274 2 T46041 hypothetical prote
989 100.5 3.2 283 2 E88597 protein Y47D38.6 [i
990 100.5 3.2 314 2 T48514 hypothetical prote
991 100.5 3.2 384 2 T50921 carbamoyl-phosphat
992 100.5 3.2 401 2 S65138 glycoprotein anti
993 100.5 3.2 440 2 JC7807 Wiskott-Aldrich sy
994 100.5 3.2 504 2 AG2373 hypothetical prote
995 100.5 3.2 504 2 S56745 mucin (clone pGM31
996 100.5 3.2 512 2 E59437 F02569.2 protein [i
997 100.5 3.2 597 2 JQ0107 hypothetical 66K p
998 100.5 3.2 677 2 T39713 zinc finger protei
999 100.5 3.2 798 2 T34248 hypothetical prote
1000 100.5 3.2 906 2 A43817 transforming prote
1001 100.5 3.2 975 2 S33121 homeotic protein C
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1004 100.5 3.2 1106 1 TVHUGL transforming prote
1005 100.5 3.2 1131 2 F96662 hypothetical prote
1006 100.5 3.2 1138 1 S24066 protein-tyrosine k
1007 100.5 3.2 1220 2 T48928 disease resistance
1008 100.5 3.2 1273 2 S58782 SEC31 protein - ye
1009 100.5 3.2 1323 2 T30253 spalt protein - mo
1010 100.5 3.2 2327 2 T42630 aggreclin - bovine
1011 100.5 3.2 2362 2 T14266 xln protein - chic
1012 100.5 3.2 3562 2 A47171 chondroitin sulfat
1013 100.5 3.2 4548 1 S00657 apoprotein(a) (EC
1014 100 3.2 230 2 A56210 neu differentiatio
1015 100 3.2 311 2 B65211 hypothetical prote
1016 100 3.2 334 2 G02409 protein kinase C-b
1017 100 3.2 366 2 S61796 T-cell-specific tr
1018 100 3.2 367 2 A33950 YopM protein - Yer
1019 100 3.2 474 2 S15921 protein TPX-VT3 -
1020 100 3.2 476 2 S39481 serum response fac
1021 100 3.2 510 2 H84824 En/Spm-like transp
1022 100 3.2 535 2 T17212 hypothetical prote
1023 100 3.2 549 2 C87719 protein R119.6 [im
1024 100 3.2 556 2 T70940 probable PPE prote
1025 100 3.2 562 2 S75308 DNA ligase (EC 6.5
1026 100 3.2 596 2 G75457 tetratricopeptide
1027 100 3.2 628 2 S44138 polyadenylate-bind
1028 100 3.2 673 2 AF1143 internalin protein
1029 100 3.2 698 2 T51915 hypothetical prote
1030 100 3.2 698 2 T17261 hypothetical prote
1031 100 3.2 699 2 T09069 probable cAMP-resp
1032 100 3.2 713 2 T44447 neuregulin-3 [limp
1033 100 3.2 725 2 T01268 leucine-rich repea
1034 100 3.2 756 2 C87432 hypothetical prote
1035 100 3.2 776 2 A46583 neuroendocrine-spe
1036 100 3.2 881 2 T01269 serine/threonine-s
1037 100 3.2 1109 2 C84545 probable disease r
1038 100 3.2 1161 2 T45294 hypothetical prote
1039 100 3.2 1182 2 I48378 hairless protein -
1040 100 3.2 1240 2 T08404 resistance complex
1041 100 3.2 1420 2 T37781 probable cytoskele
1042 100 3.2 1687 2 T30176 EGF repeat transme
1043 100 3.2 1791 2 T02345 hypothetical prote
1044 100 3.2 1802 2 T00020 bacterial blight-r
1045 100 3.2 1897 1 TDHULK leukocyte antigen-
1046 100 3.2 2459 2 AF2136 peptide synthetase
1047 99.5 3.2 108 2 S08315 cell wall protei
1048 99.5 3.2 177 2 T07642 PEARL1 protein h
1049 99.5 3.2 230 2 A44074 probable EGF-like
1050 99.5 3.2 280 2 I48713 Phox2 homeodomain
1051 99.5 3.2 293 2 C75421 hypothetical prote

99.5 3.2 352 2 S05500 Ig alpha-1 chain C
99.5 3.2 353 1 A1HU Ig alpha-1 chain C
99.5 3.2 353 1 S36438 EPRF protein - hyd
99.5 3.2 375 1 TDHUM4 monocyte surface g
99.5 3.2 383 1 VGBERG glycoprotein precu
99.5 3.2 387 2 B49175 Motch A protein -
99.5 3.2 392 2 B48423 homeotic protein e
99.5 3.2 393 1 VGBED2 glycoprotein D - h
99.5 3.2 420 2 T46910 hypothetical prote
99.5 3.2 451 2 JC4199 heat-shock protein
99.5 3.2 476 1 C70986 probable serine/th
99.5 3.2 491 2 F70699 probable pbpA prot
99.5 3.2 530 2 S52215 hypothetical prote
99.5 3.2 539 2 T28770 hypothetical prote
99.5 3.2 647 2 T43952 hypothetical prote
99.5 3.2 665 2 S62328 kinesin-like DNA b
99.5 3.2 702 2 A86383 76.4K protein kina
99.5 3.2 802 2 T24293 hypothetical prote
99.5 3.2 851 2 AD1427 internalin, probab
99.5 3.2 853 1 LJBONC neural cell adhesi
99.5 3.2 886 2 T35469 probable ATP /GTP-
99.5 3.2 903 2 T19209 probable protein k
99.5 3.2 949 2 T24294 hypothetical prote
99.5 3.2 958 2 B82994 glycine cleavage s
99.5 3.2 961 1 TSHUP4 thrombospondin 4 p
99.5 3.2 1013 2 T33470 hypothetical prote
99.5 3.2 1016 2 T41720 hypothetical prote
99.5 3.2 1056 2 A53767 mucin MUC5B, trach
99.5 3.2 1122 2 T47424 hypothetical prote
99.5 3.2 1220 2 T06403 resistance complex
99.5 3.2 1390 2 T31353 polypeptide - Arab
99.5 3.2 1473 2 T31422 C-terminal domain-
99.5 3.2 1742 2 T17120 cellulase (EC 3.2.
99 3.2 3869 2 A48205 All-1 protein +GrE
99 3.2 214 2 P00476 p15^{cas} extensin-li
99 3.2 214 2 T09854 prolina-rich cell
99 3.2 307 1 GSFF3 salivary glue prot
99 3.2 329 2 B41344 lutropin-choriogon
99 3.2 329 2 D41344 lutropin-choriogon
99 3.2 331 2 C41344 lutropin-choriogon
99 3.2 358 2 T01296 leucine-rich repea
99 3.2 415 1 A34170 acrosin (EC 3.4.21
99 3.2 428 2 S45361 LRR47 protein - fr
99 3.2 447 2 T34992 probable lipoprote
99 3.2 466 2 T06416 cysteine proteinas
99 3.2 511 2 AC0941 probable ABC trans
99 3.2 543 2 S25128 61K protein - Auto
99 3.2 564 2 I53106 gene gli protein -
99 3.2 569 2 F75381 probable two-compo
99 3.2 616 2 C75588 conserved hypothet
99 3.2 638 2 T51383 receptor protein k
99 3.2 641 2 C84726 probable receptor-
99 3.2 686 2 F96542 probable protein k
99 3.2 696 2 A41344 lutropin-choriogon
99 3.2 701 2 S61239 hypothetical prote
99 3.2 770 1 S30293 transcription fact
99 3.2 814 2 JC7389 thyroïd stimulat
99 3.2 860 2 C86203 hypothetical prote
99 3.2 940 2 H86420 probable receptor-
99 3.2 963 2 T19140 hypothetical prote
99 3.2 1000 2 C82630 serine proteinase
99 3.2 1097 2 T49187 hypothetical prote
99 3.2 1147 2 T42627 ADP-ribosylation f
99 3.2 1217 2 T52348 disease resistance
99 3.2 1317 2 T03748 apoptosis associat
99 3.2 1405 2 T04426 hypothetical prote
99 3.2 1532 2 A61262 collagen alpha 1(X
99 3.2 1538 2 E70874 probable ppsB prot
99 3.2 1694 2 S50065 sialoadhesin - mou
99 3.2 1799 1 S44920 ZK688.5 protein -
99 3.2 2029 1 TDFFLK protein-tyrosine-p
99 3.2 2088 2 E71436 hypothetical prote
99 3.2 6420 2 T30283 polyketide synthas

1125	98.5	3.1	230	2	T22763	hypothetical prote	1198	97.5	3.1	362	2	S22395	fetuin precursor -
1126	98.5	3.1	254	2	D88560	protein F58A4.1 [i	1199	97.5	3.1	429	2	JC4965	elk1 proteinal - mou
1127	98.5	3.1	342	2	I77461	luteinizing hormon	1200	97.5	3.1	460	2	T23087	hypothetical prote
1128	98.5	3.1	349	2	T15422	hypothetical prote	1201	97.5	3.1	464	2	S22697	extensin - Volvox
1129	98.5	3.1	379	2	S50125	larval glue protei	1202	97.5	3.1	497	2	F83634	hypothetical prote
1130	98.5	3.1	385	2	T18180	proline-rich prote	1203	97.5	3.1	511	2	T43282	alpi1 proteinal - fi
1131	98.5	3.1	393	2	S62335	hypothetical prote	1204	97.5	3.1	521	2	S50466	glycoprotein gc -
1132	98.5	3.1	434	1	A35005	u-plasminogen acti	1205	97.5	3.1	531	2	B55066	tyrosine decarboxy
1133	98.5	3.1	464	2	D72653	hypothetical prote	1206	97.5	3.1	563	2	A75594	ferredoxin-nitrite
1134	98.5	3.1	486	2	B39481	serum response fac	1207	97.5	3.1	574	1	A48501	probable protein-1
1135	98.5	3.1	514	2	A44100	cell adhesion mole	1208	97.5	3.1	587	2	T41653	probable transcrip
1136	98.5	3.1	633	2	T47346	receptor protein k	1209	97.5	3.1	614	2	T33149	hypothetical prote
1137	98.5	3.1	700	2	I77463	luteinizing hormon	1210	97.5	3.1	626	2	B70754	probable serine/th
1138	98.5	3.1	700	2	A49744	lutropin-choriogon	1211	97.5	3.1	627	1	JC6534	protein kinase 1 (
1139	98.5	3.1	707	2	A46302	PTB-associated spl	1212	97.5	3.1	627	2	AB0535	hypothetical prote
1140	98.5	3.1	770	2	T22808	hypothetical prote	1213	97.5	3.1	631	1	A36749	transcription fact
1141	98.5	3.1	803	2	F59433	RhOGAP protein [im	1214	97.5	3.1	662	2	D40228	neurexin II-beta p
1142	98.5	3.1	837	2	A42112	mucin-like peptide	1215	97.5	3.1	676	1	EDBE23	immediate-early pr
1143	98.5	3.1	862	2	B88594	protein Y48A68.11	1216	97.5	3.1	710	2	D96728	hypothetical prote
1144	98.5	3.1	885	2	B86257	NBS/LRR disease re	1217	97.5	3.1	754	2	AC2807	OmpA family protei
1145	98.5	3.1	921	2	D86293	F7H2.22 protein -	1218	97.5	3.1	754	2	B97586	hypothetical prote
1146	98.5	3.1	947	2	T26314	hypothetical prote	1219	97.5	3.1	814	2	G02390	disintegrin-like m
1147	98.5	3.1	1087	2	T31100	probable potassium	1220	97.5	3.1	817	2	S51342	verprolin - yeast
1148	98.5	3.1	1272	2	T30248	fragile X mental r	1221	97.5	3.1	830	2	T17672	chitinase-like pro
1149	98.5	3.1	1281	2	T00346	hypothetical prote	1222	97.5	3.1	893	2	H96651	protein T3P18.19 [
1150	98.5	3.1	1309	2	T00078	probable RNA-direc	1223	97.5	3.1	909	1	A54809	disease resistance
1151	98.5	3.1	1396	2	A44453	translation initia	1224	97.5	3.1	921	2	AE0332	conserved hypothet
1152	98.5	3.1	1774	2	B56101	collagen alpha 1(X	1225	97.5	3.1	929	2	T52517	hypothetical prote
1153	98.5	3.1	2180	2	T29764	hypothetical prote	1226	97.5	3.1	948	2	F87693	peptidase, M16 fam
1154	98.5	3.1	2339	2	A42566	omega-conotoxin-se	1227	97.5	3.1	1006	2	G86292	hypothetical prote
1155	98	3.1	182	2	T07641	PEARL1 protein h	1228	97.5	3.1	1258	2	JC5765	inositol polyphosp
1156	98	3.1	291	2	AF0123	probable antigenic	1229	97.5	3.1	1392	2	T51947	probable transcrip
1157	98	3.1	296	2	A56943	sensory/motor neur	1230	97.5	3.1	1715	2	C40228	neurexin II-alpha
1158	98	3.1	303	2	S40973	hypothetical prote	1231	97.5	3.1	1748	1	J01555	genome polyprotein
1159	98	3.1	352	2	S09266	Ig alpha chain C r	1232	97	3.1	191	2	F84522	probable proline-r
1160	98	3.1	416	1	A42879	advanced glycosyla	1233	97	3.1	238	2	T23867	hypothetical prote
1161	98	3.1	442	2	S50062	cell wall glycopro	1234	97	3.1	238	2	T26419	hypothetical prote
1162	98	3.1	499	2	A12449	hypothetical prote	1235	97	3.1	330	2	T05717	probable extensin
1163	98	3.1	514	2	A56201	transcription fact	1236	97	3.1	355	2	B26883	neural cell adhesi
1164	98	3.1	534	2	S21961	proline-rich prote	1237	97	3.1	357	2	A39364	GDF-1 embryonic gr
1165	98	3.1	535	2	S65762	chitinase (EC 3.2.	1238	97	3.1	379	2	AE3003	conserved hypothet
1166	98	3.1	538	2	I68093	PRR2 delta - human	1239	97	3.1	395	2	A86166	protein F21B7.6 [i
1167	98	3.1	538	2	A70836	hypothetical prote	1240	97	3.1	397	2	T00914	leucine-rich repea
1168	98	3.1	553	1	A42499	mullerian inhibiti	1241	97	3.1	400	1	A28172	spasmolysin precu
1169	98	3.1	560	1	WFH0M	mullerian inhibiti	1242	97	3.1	421	1	S11674	acrosin (EC 3.4.21
1170	98	3.1	605	2	S48940	hypothetical prote	1243	97	3.1	428	1	TVHUEK	transforming prote
1171	98	3.1	614	2	S27962	modulator recognit	1244	97	3.1	452	2	D98280	hypothetical 28.0K
1172	98	3.1	631	2	C89243	protein F28C1.3 [i	1245	97	3.1	459	2	T35317	probable serine/th
1173	98	3.1	631	2	T21471	hypothetical prote	1246	97	3.1	483	2	T02226	NBS-LRR type resis
1174	98	3.1	715	2	S76492	lipoprotein nlpD -	1247	97	3.1	500	2	D97302	hypothetical prote
1175	98	3.1	728	2	H59435	phosphoinositide-3	1248	97	3.1	530	2	G70904	hypothetical prote
1176	98	3.1	750	2	T42614	probable envelope	1249	97	3.1	601	2	D89711	protein F40E10.4 [
1177	98	3.1	788	1	Q3BEE3	HLHFI protein - hu	1250	97	3.1	601	2	T22025	hypothetical prote
1178	98	3.1	856	2	T43631	serine/threonine k	1251	97	3.1	632	2	T02627	hypothetical prote
1179	98	3.1	889	2	C86257	resistance to Pseu	1252	97	3.1	701	1	FCV1LR	gag polyprotein -
1180	98	3.1	896	2	S36326	clathrin assembly	1253	97	3.1	860	2	JC4566	chitinase (EC 3.2.
1181	98	3.1	1006	2	JC5526	kinase-defective E	1254	97	3.1	966	2	D96662	hypothetical prote
1182	98	3.1	1216	2	T34101	hypothetical prote	1255	97	3.1	967	2	G96637	hypothetical prote
1183	98	3.1	1372	2	T25933	hypothetical prote	1256	97	3.1	1123	2	A39962	kinase-related tra
1184	98	3.1	1522	2	H88380	protein T22F7.3 [i	1257	97	3.1	1214	2	T47438	disease resistance
1185	98	3.1	1873	2	A55645	calcium channel, v	1258	97	3.1	1265	1	A37967	neural cell adhesi
1186	98	3.1	2115	2	S38480	nonstructural prot	1259	97	3.1	1690	2	T35694	ATP dependent DNA
1187	98	3.1	3190	2	T13828	CREB-binding prote	1260	97	3.1	1734	2	A54602	microtubule-associ
1188	98	3.1	3623	2	T08618	intrinsic factor-B	1261	97	3.1	2055	2	T00093	hypothetical prote
1189	98	3.1	3635	2	T10053	laminin alpha 5 ch	1262	97	3.1	2205	1	GNNY2W	genome polyprotein
1190	98	3.1	3871	2	T22812	hypothetical prote	1263	97	3.1	3034	2	T14119	seven-pass transme
1191	98	3.1	5069	2	T17464	rifamycin polyketi	1264	96.5	3.1	346	2	S19129	proline-rich prote
1192	97.5	3.1	215	2	S55925	probable arabinoga	1265	96.5	3.1	350	2	E75341	peptidyl-prolyl ci
1193	97.5	3.1	266	1	A35037	insulin-like growt	1266	96.5	3.1	419	2	G70602	hypothetical prote
1194	97.5	3.1	268	2	S71830	transcription coac	1267	96.5	3.1	430	2	I48755	mSAPla - mouse
1195	97.5	3.1	277	2	A46241	interferon respons	1268	96.5	3.1	444	2	B36389	transcription fact
1196	97.5	3.1	306	2	T09067	extensin-like prot	1269	96.5	3.1	485	1	S22543	transcription fact
1197	97.5	3.1	338	1	TVM5FB	transforming prote	1270	96.5	3.1	487	2	F70765	hypothetical prote

1271	96.5	3.1	514	2	A31643	cell adhesion 80k	1344	95.5	3.0	1159	2	I38465	probable potassium
1272	96.5	3.1	528	2	B75310	conserved hypother	1345	95.5	3.0	1255	2	T31065	diaphanous protein
1273	96.5	3.1	574	2	B35149	ipah protein - Shi	1346	95.5	3.0	1256	2	T30396	CDO protein - rat
1274	96.5	3.1	598	2	T42070	protein serine/thr	1347	95.5	3.0	1331	2	T49813	related to gastrin
1275	96.5	3.1	635	2	F70874	probable membrane	1348	95.5	3.0	1630	2	T00390	KIAA0614 protein -
1276	96.5	3.1	637	2	A75342	hypothetical prote	1349	95.5	3.0	2761	2	T21064	hypothetical prote
1277	96.5	3.1	646	2	T34532	hypothetical prote	1350	95	3.0	175	2	I38408	neu differentiation
1278	96.5	3.1	654	2	T45017	chemotaxis histidi	1351	95	3.0	227	2	C29149	proline-rich prote
1279	96.5	3.1	669	2	T08827	hypothetical prote	1352	95	3.0	227	2	G70555	hypothetical prote
1280	96.5	3.1	796	2	E96654	hypothetical prote	1353	95	3.0	239	2	S25618	hypothetical prote
1281	96.5	3.1	825	1	EDBEXD	immediate-early pr	1354	95	3.0	241	2	D43273	heregulin precuro
1282	96.5	3.1	1021	2	A86421	Receptor-like seri	1355	95	3.0	273	2	C70551	hypothetical prote
1283	96.5	3.1	1209	2	T00373	hypothetical prote	1356	95	3.0	326	2	A59232	ABA-responsive pro
1284	96.5	3.1	1241	2	T18311	hypothetical prote	1357	95	3.0	338	2	T06336	proline-rich prote
1285	96.5	3.1	1557	2	T02859	probable serine/th	1358	95	3.0	385	1	I39498	GTP cyclohydrolase
1286	96.5	3.1	2282	2	T42717	DNA-binding protei	1359	95	3.0	413	2	T52617	hypothetical prote
1287	96.5	3.1	2352	2	T30201	Notch homolog prot	1360	95	3.0	477	2	S53362	mucin 5AC (clone J
1288	96.5	3.1	26926	1	I38344	titin, cardiac mus	1361	95	3.0	494	1	A29079	lymphocyte surface
1289	96	3.1	214	2	T10737	extensin-like cell	1362	95	3.0	502	2	A55197	Wiskott-Aldrich sy
1290	96	3.1	240	2	A24264	proline-rich prote	1363	95	3.0	636	2	I61718	neu differentiation
1291	96	3.1	287	2	T75494	cell division prote	1364	95	3.0	653	2	E84682	hypothetical prote
1292	96	3.1	346	2	JA0159	cysteine proteinas	1365	95	3.0	662	2	I61722	neu differentiation
1293	96	3.1	445	2	T05887	hypothetical prote	1366	95	3.0	667	2	T17221	hypothetical prote
1294	96	3.1	451	2	D88395	protein P53A3.6 li	1367	95	3.0	673	2	T48012	hypothetical prote
1295	96	3.1	483	2	S12741	transcription fact	1368	95	3.0	705	2	A35621	spore germination
1296	96	3.1	537	1	FOWGVV	gag polyprotein -	1369	95	3.0	712	2	G02512	interleukin-1 rece
1297	96	3.1	580	2	T43481	probable mucin DKF	1370	95	3.0	760	2	T16726	hypothetical prote
1298	96	3.1	594	2	S33561	ref(2)P protein -	1371	95	3.0	776	2	C96554	unknown protein li
1299	96	3.1	598	2	T48822	hypothetical prote	1372	95	3.0	799	2	T48889	serine/threonine p
1300	96	3.1	635	1	WMBE66	capsid protein - h	1373	95	3.0	846	2	S52418	GTP-binding regula
1301	96	3.1	858	1	IJRTNC	neural cell adhesi	1374	95	3.0	891	2	G84693	probable proline-r
1302	96	3.1	883	2	A96662	hypothetical prote	1375	95	3.0	901	2	A44825	phosphoprotein, sy
1303	96	3.1	907	2	AD2951	cell division prot	1376	95	3.0	903	2	S60257	meltrin alpha - mo
1304	96	3.1	910	2	H98331	McxB-related prote	1377	95	3.0	943	2	T34847	probable transcript
1305	96	3.1	969	2	A75634	hypothetical prote	1378	95	3.0	1024	2	S18251	collagen alpha 1(X
1306	96	3.1	1216	2	T26104	hypothetical prote	1379	95	3.0	1209	2	T13153	brahma associated
1307	96	3.1	1231	2	S30185	insulin receptor s	1380	95	3.0	1324	2	T14070	peptide synthetase
1308	96	3.1	1344	2	E59431	phosphoinositide-b	1381	95	3.0	1474	2	B85188	retrotransposon li
1309	96	3.1	1615	2	B49502	protein-tyrosine-p	1382	95	3.0	1616	2	G70668	polyketide synthas
1310	96	3.1	1737	2	T02029	MEGF8 protein - hu	1383	95	3.0	1731	2	AB3045	ice nucleation pro
1311	96	3.1	1767	2	I49502	protein-tyrosine-p	1384	95	3.0	1731	2	B98241	hypothetical prote
1312	96	3.1	1844	1	RRWPTM	genome polyprotein	1385	95	3.0	1770	2	T18551	saframycin Mxi syn
1313	96	3.1	2529	2	A56923	transcription fact	1386	95	3.0	1806	1	CGHUE	collagen alpha 1(X
1314	96	3.1	5376	2	T42215	zonadhesin - mouse	1387	95	3.0	2090	2	T30075	hypothetical prote
1315	95.5	3.0	188	2	D29149	proline-rich prote	1388	95	3.0	2148	2	A56011	transcription fact
1316	95.5	3.0	284	2	F95320	conserved hypother	1389	95	3.0	2274	2	T30258	adenomatous polyo
1317	95.5	3.0	366	1	TDMSM4	monocyte surface g	1390	95	3.0	3084	1	MMWSA	laminin alpha-1 ch
1318	95.5	3.0	382	2	S75823	threonine synthase	1391	94.5	3.0	211	2	T03381	high sulfur zein p
1319	95.5	3.0	384	2	S51796	vasodilator-stimul	1392	94.5	3.0	255	2	B75309	hypothetical prote
1320	95.5	3.0	435	2	T46443	hypothetical prote	1393	94.5	3.0	255	2	S31096	proline-rich prote
1321	95.5	3.0	451	2	S71754	cellular hepatitis	1394	94.5	3.0	270	2	E87649	hypothetical prote
1322	95.5	3.0	479	2	D70676	probable PE protei	1395	94.5	3.0	277	2	I38857	microtubule-associ
1323	95.5	3.0	486	2	AB2975	succinate semialde	1396	94.5	3.0	298	2	H87533	peptidase, M23/M37
1324	95.5	3.0	486	2	A98308	atcK protein (U594	1397	94.5	3.0	301	2	D87684	transcription regu
1325	95.5	3.0	501	2	S75563	hypothetical prote	1398	94.5	3.0	358	2	A61188	probable transcript
1326	95.5	3.0	507	1	A46713	erythropoietin rec	1399	94.5	3.0	376	2	H82988	hypothetical prote
1327	95.5	3.0	553	2	C75318	hypothetical prote	1400	94.5	3.0	393	2	E82283	conserved hypother
1328	95.5	3.0	570	2	A48836	fibropallin C prec	1401	94.5	3.0	464	2	A83557	probable amidase P
1329	95.5	3.0	571	2	T43456	hypothetical prote	1402	94.5	3.0	569	2	T19128	hypothetical prote
1330	95.5	3.0	573	2	B70726	probable secD - My	1403	94.5	3.0	630	2	A39344	tumor-associated m
1331	95.5	3.0	624	2	T49366	myocyte-specific e	1404	94.5	3.0	665	2	E75461	probable cell wall
1332	95.5	3.0	630	2	T31798	hypothetical prote	1405	94.5	3.0	708	2	JC4364	gelatinase B (EC 3
1333	95.5	3.0	650	2	S44806	F10E9.6 protein -	1406	94.5	3.0	719	2	T33170	hypothetical prote
1334	95.5	3.0	685	2	C56591	E75 B steroid rece	1407	94.5	3.0	860	2	I48839	tenascin-X - mouse
1335	95.5	3.0	710	1	S70965	serine/threonine-s	1408	94.5	3.0	921	2	S42617	collagen alpha 1(I
1336	95.5	3.0	722	2	T22359	hypothetical prote	1409	94.5	3.0	985	2	T06049	hypothetical prote
1337	95.5	3.0	749	2	E87599	hypothetical prote	1410	94.5	3.0	1006	2	T00050	hypothetical prote
1338	95.5	3.0	790	1	TVHUTT	nerve growth facto	1411	94.5	3.0	1092	1	JN0635	neural cell adhesi
1339	95.5	3.0	880	2	D89756	protein T23E7.2b l	1412	94.5	3.0	1191	2	T13850	gene u-shaped prot
1340	95.5	3.0	943	2	E84429	probable receptor-	1413	94.5	3.0	1487	1	EDBEE1	immediate-early pr
1341	95.5	3.0	987	2	A54092	protein-tyrosine k	1414	94.5	3.0	1690	1	CGHUIB	collagen alpha 4(I
1342	95.5	3.0	1027	2	I38759	zinc finger/leucin	1415	94.5	3.0	2062	2	G96602	probable receptor
1343	95.5	3.0	1054	2	A30239	hydroxymethylgluta	1416	94.5	3.0	2302	2	T14328	protein-tyrosine-p

A;Cross-references: UNIPROT:P35858; UNIPARC:UPI000000088A; GB:M86826; NID:g184807; PIDN:

A;Experimental source: liver

A;Note: sequence extracted from NCBI backbone (NCBIP:110171)

F;75-98/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>

F;99-122/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>

F;123-146/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>

F;147-170/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>

F;171-194/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>

F;195-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>

F;219-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>

F;243-266/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>

F;267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>

F;291-314/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>

F;315-338/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>

F;339-362/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>

F;363-386/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>

F;387-410/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>

F;411-434/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>

F;435-458/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR16>

F;459-482/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR17>

F;483-506/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR18>

F;507-529/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR19>

Query Match 9.6%; Score 302; DB 2; Length 605;

Best Local Similarity 35.5%; Pred. No. 2.9e-10;

Matches 98; Conservative 40; Mismatches 98; Indels 40; Gaps 11;

QY 7 LLLPLLLL-LALG-----PGVQG-----CPSGCQCSQPQ-----TFVCTARQGT 45

Db 8 LALALLLSWALPGSRLEAGDPGTGGEAGPACPAACVCSYDDADELSVCSSRNLTR 67

QY 46 VPRDVPDVTGLVYFENGITMLDASSFAGLPGLQLLDLSQNIASIRLPRILL----- 98

Db 68 LPDGVPGGTQALWLDGNLSSVPPFAFQNLSSLSGLFNLQGGQLGSLF-PQALLGLENLCH 126

QY 99 LDLSHNSLLALEPGLDITANVEALRLAGLG--LQQLDEGLFSRLNLHLDVDSNQLER 155

Db 127 LHLERNQLRSALGTF--AHTPALASLGLSNRLSRLEDGLPEGLGSLWDLNLGWSLAV 184

QY 156 VP-PVIRGLRGTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLPFR 214

Db 185 LPDAAFRGLSGLSRELVLAGN-RLAVLPALFSGIAELRELDLSRNALRAIKANVFVQLPR 243

QY 215 LRLLAAARNPFCVPLSWFG----PWRESHVTLA 246

Db 244 LQKLYLDRNLIAAVAPGAFGLKALRWLDLSHRVA 279

RESULT 3

NBHUA

platelet glycoprotein Ib alpha chain precursor - human

N;Alternate names: membrane glycoprotein Ib alpha chain

N;Contains: glycoocalicin

C;Species: Homo sapiens (man)

C;Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #text change 09-Jul-2004

C;Accession: A94174; A60435; A94173; S16945; I55355; A27075; A27102

R;Lopez, J.A.; Chung, D.W.; Fujikawa, K.; Hagen, F.S.; Papayannopoulou, T.; Roth, G.J.

Proc. Natl. Acad. Sci. U.S.A. 84, 5615-5619, 1987

A;Title: Cloning of the alpha-chain of human platelet glycoprotein Ib: a transmembrane p

A;Reference number: A94174; MUID:87289655; PMID:3303030

A;Accession: A94174

A;Molecule type: mRNA

A;Residues: 1-626 <LQ>

A;Cross-references: UNIPROT:P07359; UNIPARC:UPI000012B962; GB:J02940; NID:g183499; PIDN:

R;Wicki, A.N.; Walz, A.; Gerber-Huber, S.N.; Wenger, R.H.; Vornhagen, R.; Clemetson, K.J

Thromb. Haemost. 61, 448-453, 1989

A;Title: Isolation and characterization of human blood platelet mRNA and construction of

d cloning of a GPIb coding cDNA insert.

A;Reference number: A60435; MUID:90020160; PMID:2799758

A;Accession: A60435

A;Molecule type: mRNA

A;Residues: 207-467 <WIC>

A;Cross-references: UNIPARC:UPI0000174311

R;Titani, K.; Takio, K.; Handa, M.; Ruggeri, Z.M. Proc. Natl. Acad. Sci. U.S.A. 84, 5610-5614, 1987									
A;Title: Amino acid sequence of the von Willebrand factor-binding domain of platelet membrane protein									
A;Reference number: A94173; MUID:87289654; PMID:3497398									
A;Accession: A94173									
A;Molecule type: protein									
A;Residues: 17-315 <TIT>									
A;Cross-references: UNIPARC:UPI0000174312									
R;Hess, D.; Schaller, J.; Rickli, E.E.; Clemetson, K.J. Eur. J. Biochem. 199, 389-393, 1991									
A;Title: Identification of the disulphide bonds in human platelet glycoocalicin.									
A;Reference number: S16945; MUID:91301149; PMID:2070794									
A;Accession: S16945									
A;Status: preliminary									
A;Molecule type: protein									
A;Residues: 224-227;262-270;277-282 <HES>									
A;Cross-references: UNIPARC:UPI0000174313; UNIPARC:UPI0000174314; UNIPARC:UPI0000174315									
R;Lopez, J.A.; Ludwig, E.H.; McCarthy, B.J. J. Biol. Chem. 267, 10055-10061, 1992									
A;Title: Polymorphism of human glycoprotein Ib alpha results from a variable number of tandem repeats									
A;Reference number: I55355; MUID:92250564; PMID:1577776									
A;Accession: I55355									
A;Status: preliminary; translated from GB/EMBL/DBJ									
A;Molecule type: DNA									
A;Residues: 412-427 <RES>									
A;Cross-references: UNIPARC:UPI0000073621; GB:S34436; NID:g249176; PIDN:AAB22152.1; PID:155355									
A;Note: variant D									
C;Comment: Glycoprotein Ib (GPIb), a surface membrane protein of platelets, participates in platelet adhesion and aggregation									
C;Comment: Platelet activation apparently involves disruption of the macromolecular complex									
C;Comment: Binding sites for von Willebrand factor and thrombin (the latter site with unique amino acid sequence)									
C;Comment: Glycoocalicin, which is approximately coextensive with the extracellular part of the protein									
C;Genetics:									
A;Gene: GDB:GP1BA; GPIB									
A;Cross-references: GDB:118906; OMIM:231200									
A;Map position: 17pter-17p12									
C;Complex: heterodimer with platelet glycoprotein Ib beta chain (NBHUIB)									
C;Superfamily: platelet glycoprotein Ib alpha chain; leucine-rich alpha-2-glycoprotein repeat									
C;Keywords: blood coagulation; duplication; glycoprotein; platelet membrane; tandem repeat									
F;1-16/Domain: signal sequence #status predicted <SIG>									
F;17-626/Product: platelet glycoprotein Ib alpha chain #status predicted <MPT>									
F;48-71/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>									
F;72-93/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>									
F;94-116/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>									
F;117-140/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>									
F;141-164/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>									
F;165-188/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>									
F;189-212/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>									
F;379-430/Region: proline/threonine-rich 9-residue repeats									
F;502-540/Domain: transmembrane #status predicted <TRM>									
F;541-626/Domain: intracellular #status predicted <INT>									
F;37,175/Binding site: carbohydrate (Asn) (covalent) #status experimental									
F;308/Binding site: carbohydrate (Thr) (covalent) #status experimental									
Query Match									
Best Local Similarity 9.0%; Score 282; DB 1; Length 626;									
Matches 160; Conservative 72; Mismatches 244; Indels 190; Gaps 26;									
Qy	9	LPLLLLLALPGVGQCPGCGCQSQPQT---VFCTAQGTTPVRDVPDPTVGLYVFEN---	62						
Db	1	MPLLLLLLLPSPLGALRGELQEL							

Matches 127; Conservative 56; Mismatches 207; Indels 102; Gaps 16;	
QY	6 PLLLLPLLLLLALPGVQGCSCQSQPOTVCTARQGTTPRDVPPDTVGLVYFENGIT 65
Db	16 PELWLLWAAAWRLGATACPALCTCT-GTVDCHGTGLQAIKNTPRNTERLELGNMIT 74
QY	66 MLDASSFAGLPGQLQLDLSQNGIASLRPLRLLELLDLSHNSLLALEPGIL-DYANVEALRL 124
Db	75 RIHKNDFAGLKQLRVQLMENOIG-----AVERGAFDDMKELERLRL 116
QY	125 AGLGLQQLDEGLFSRLRNLDLVDSDNQLRVP-PVIRGLRGLRLRLAGNTRIAQLRPE 183
Db	117 NRNQLVLPPELLFQNNQALSRDLSENLSQAVPRKAFGATDLKNLQDKN-QISCIEEG 175
QY	184 DIAGLAALQELDVNSLSQALPGDLISGLFPRRLRLAAARNPNCVCPISWFGPWVRESHV 243
Db	176 AFRALRGLEVLTLNNNITTPVSNFNMHPKLRTRFLHSNHLFCDCHLAWLSQWLQ-RP 234
QY	244 TLASPEETRCFPKPNAGRLLELDYADGCPATTTTATVPTTRPVVREPTALSSSLAPT 303
Db	235 TIGL--FTCCSGPASIRGUNVAEVOKSEFSCSGQGEAAQVPA-----CTLSSGSCPA 284
QY	304 WLSPTAPATEAPSPSTAPPTVGPVPQO-----DCPSTCLNGGTCHLG----- 348
Db	285 MCSCSNGIIVDCRGKGLTAIPANLPETMTETIRLELNGIKSIPP-----GAFSPYR 333
QY	349 -----TRHHLACLPBGFTGLCYESQMGQSTRSPPTVTPRPRSLTLGIEPVS--PT 399
Db	334 KLRRIDLSSNOIAEAPAFQGL-----RSLNSLVLYGNKITDLP 374
QY	400 SURVGLQRYLQSGSQVLSRLTRYLNSGPD--KRLVTLRLPA-----SLAEYTVTQL 450
Db	375 GVFGGLY-----TLQLLLLNANKINCIRPDFAQDLQNLSSLSLYDNKIQSLAKGFTTSL 428
QY	451 RPNATYSCVCMWP 462
Db	429 RAIQTLHLAQN 440
RESULT 7	
A:Accession: A53531	
N:Alternate names: oncofetal antigen 574	
C:Species: Homo sapiens (man)	
C>Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004	
R:Myers, K.A.; Rahi-Saund, V.; Davison, M.D.; Young, J.A.; Cheater, A.J.; Stern, P.L.	
J. Biol. Chem. 269, 9319-9324, 1994	
A:Title: Isolation of a cDNA encoding 574 oncofetal trophoblast glycoprotein. An antigen	
A:Reference number: A53531; MUID:94179356; PMID:8132670	
A:Accession: A53531	
A>Status: preliminary	
A:Molecule type: mRNA	
A:Residues: 1-420 <MEY>	
A:Cross-references: UNIPROT:Q13641; UNIPARC:UPI000004CAD5; EMBL:229083; NID:G435654; PID	
F:1-31/Domain: signal sequence #status predicted <SIG>	
F:32-420/Product: oncofetal trophoblast glycoprotein 574 #status predicted <MAT>	
Query Match 8.4%; Score 264.5; DB 2; Length 420;	
Best Local Similarity 28.1%; Pred. No. 2.9e-08;	
Matches 103; Conservative 44; Mismatches 121; Indels 99; Gaps 15;	
QY	2 CSRVP-----LLPLLLLLAALG-----PGVQCPS 26
Db	5 CSRGAAGDGRLLARLALVLIGVSSSSPTSSASSFSAPFLASAVSAQPLPDQCPA 64
QY	27 GCQCSQ-PQTVECTARQGTTPRDVPPDTVGLVYFENGITMLDASSFAGLP---GLQLLD 82
Db	65 LCECEAAATVKVNRNITEVETDLPAYVRNLFITGNQLAVLPAGAFARPPPLAEALN 124
QY	83 LSONQIASLR-----LPRLLLDLSHNSLLALEPGILDANVEALRLAGLQQLDEGL 136

Db	125 LSGSRLDEVAGAPEHLPSLRQLDLSHNPLADLSPPAFSGSNASV-----SAPSPL 175
QY	137 FSLRLNLDLVDSDNQLR-----VPPVI--RGLRGLTRLRLAGNTRIAQLRPDLAQL 188
Db	176 VELILN-HIVPPEDERQNRSEFGMVVAALLAGRALQGLRRLLELASN-HFLYLPDRVLAQL 233
QY	189 AALQELDVNSLSQALP-----GDLISGLPFPRLRLAA 220
Db	234 PSRLRLDLSNNSLVSLTIVSPRNLTLSLHLEDNALKVLHNGTTLAEQGL-PIRVF-L 291
QY	221 ARNPNCVCPISWFGPWVRESHVTLASPEETRCFPKPNAGRLLELDYADFGC---PA 276
Db	292 DNNPWCDCMADVMVTLKETEV-VQKDRLTCAYPEKWRNVRVLELASADLDCDPIPPP 350
QY	277 TTTTATV 283
Db	351 SLQTSYV 357
RESULT 8	
MEGF5 protein - rat	
N:Alternate names: slit protein homolog	
C:Species: Rattus norvegicus (Norway rat)	
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004	
C:Accession: T13953	
R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.	
Genomics 51, 27-34, 1998	
A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs	
A:Reference number: Z14126; MUID:98360089; PMID:9693030	
A:Accession: T13953	
A>Status: preliminary; translated from GB/EMBL/DBJ	
A:Molecule type: mRNA	
A:Residues: 1-1523 <NAK>	
A:Cross-references: UNIPROT:O88280; UNIPARC:UPI000000E5F7A; EMBL:AB011531; NID:G3449291;	
C:Genetics:	
A:Gene: MEGF5	
C:Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein	
Query Match 8.3%; Score 261; DB 2; Length 1523;	
Best Local Similarity 26.3%; Pred. No. 2e-07;	
Matches 93; Conservative 41; Mismatches 126; Indels 94; Gaps 14;	
QY	24 CPSCQCSQPTVCTARQGTTPRDVPPDTVGLVYFENGITMLDASSFAGLPGLQLLDL 83
Db	725 CPEQCTCYE-TVVRCNSRGLHTLPKGMKDVTELYLEGNHLTAV----- 767
QY	84 SONOIASLRPLRLLDLSHNSLLALEPGILDANVEALRLAGLQQLDEGLFSRLRL 143
Db	768 -PKELSTFR--QLTLIDLSNNS-----ISMLTHTFTSNMSHL 801
QY	144 HDLVDSDNQLRVP-PVIRGLRGLTRLRLAGNTRIAQLRPDLAQLAALQELDVNSLSQ 202
Db	802 STLILSYNLRACIPVHAFENGLRSLRVLTLHGN-----DISSVPEGSFNDLTSL-- 850
QY	203 ALPGDLSGLFPRRLRLAAARNPNCVCPISWFGPWVRESHVTLASPETRCHFPKPNAGR 262
Db	851 -----HLALGINPLHCDCSLRSLSEWIKAGY---KEPFIARCSSPESMADR 893
QY	263 LLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLAPTTLSPATAPATEAPSPSTAP 322
Db	894 LLLTPTTHRFQCKG-----PVDINIVAKNACLSS--PCKNNGTCSQDPVEQVRCRCP 944
QY	323 PTVGFPVPODPC--PPSTCL-----NGGCTHLGTRHH--LACLCPEGFTGLYCE 367
Db	945 YSY----KGKDTVPINTCVQNPQCHGTCHLSHRDGFSCSCPLGEGQRC 994
RESULT 9	
B36665	
slit protein 2 precursor - fruit fly (Drosophila melanogaster)	
C:Species: Drosophila melanogaster	
C>Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 02-Aug-2002	

C;Accession: B36665
R;Rothberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.
Genes Dev. 4, 2169-2187, 1990
A;Title: slit: an extracellular protein necessary for development of midline glia and cell
A;Reference number: A36665; MUID: 91099665; PMID: 2176636
A;Accession: B36665
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1469 <ROT>
A;Cross-references: UNIPARC:UPI0000177454; GB:X53959
C;Gene: FlyBase:slit
A;Cross-references: FlyBase:FBgn0003425
C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein x
F;66-91/Domain: proteoglycan amino-terminal homology <PAH1>
F;101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;197-220/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;228-272/Domain: proteoglycan carboxyl-terminal homology <PCS1>
F;288-313/Domain: proteoglycan amino-terminal homology <PAH2>
F;323-346/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;347-370/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;395-418/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F;419-442/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>
F;450-494/Domain: proteoglycan carboxyl-terminal homology <PCS2>
F;512-537/Domain: proteoglycan amino-terminal homology <PAH3>
F;547-571/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>
F;572-595/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>
F;596-619/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>
F;620-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>
F;651-695/Domain: proteoglycan carboxyl-terminal homology <PCS3>
F;708-733/Domain: proteoglycan amino-terminal homology <PAH4>
F;743-766/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>
F;767-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR16>
F;846-890/Domain: proteoglycan carboxyl-terminal homology <PCS4>
F;1028-1061/Domain: EGF homology <EGF>
F;1068-1099/Domain: EGF homology <EGF2>
F;1115-1148/Domain: EGF homology <EGF1>
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Best Local Similarity 21.4%; Pred. No. 3.9e-07;
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DB 519 CPAMCHC-EGTTVDCGTGRLEKIPRIDPLHTTELLNDNELGRISDGLFGRPLHLVKLE 577
QY 59 VPENGITMLDASSFAGLPGQLLDLSONOIAS-----LRLPRLLLLDLSHNSLLALEPG 112
DB 578 LKRNQUTGIEPNAFEGASHIQELQGENKIKISNOMFGLGHQTKTLNLYDNOISCVMPG 637
QY 113 ILDTAN-----VEALRLAGLGLQQLDEGLFSRLRNLDLHDV--- 148
DB 638 SPEHLNLSLNLASPNFNCNLHAWFAECVRKKSINGGAACGAPSKVRDVQIKDLPHS 697
QY 149 -----SDNQLRVP-----PV----- 159
DB 698 EFKCSSENSEGLGDGCGPFCSTCTGTVVACSRNQLKEIPRGIPAEYSLEYESNEIQI 757
QY 160 ----TRELGLTRLAGNTRIAQLRPEDLAGLAALQELDVS-----NL 199
DB 758 HYERIKHLSLFRDLDS-NNQITILSNYTFANLTKLSTLIISYNKLCQLQRHALSGLNNL 816
QY 200 SLQALPGDLSGLFPR-----LRLAAARNPFCNCVPLSFGFWVRESHYVTLASPBE 251
DB 817 RVVSLHGNISMLPEGSFEDLKSLLTHIALGNSPLYCDCLGWFSWDIKLDV---EPGIA 873
QY 252 RCHFPKNGRLLLELDYADFQCPATTTATVTPTRPVVREPTALSSSLAPWLSFTAPA 311
DB 874 RCAEPEQMKDKLILSTPSSSFVCRGVRNDILAKCNACFEQPCQNAOCV-----ALPQ 927

QY 312 TEAPSPPTAPPTVGVFPQP-----QDCPSTCLNGTCHLGRHHLACLCPG 360
DB 928 REVQC-----LCQFGVGHKCEPMIDACYGNPCNNATCTVLEGRFSCQCAPG 976
QY 361 FTGLYCESQM 370
DB 977 YTGARCETNI 986

RESULT 10

A36665
slit protein 1 precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 30-Apr-1991 #sequence revision 30-Apr-1991 #text_change 02-Aug-2002
C;Accession: A36665; A31640; S13523
R;Rothberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.
Genes Dev. 4, 2169-2187, 1990
A;Title: slit: an extracellular protein necessary for development of midline glia and cell
A;Reference number: A36665; MUID: 91099665; PMID: 2176636
A;Accession: A36665
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1480 <ROT>
A;Cross-references: UNIPARC:UPI0000150FD1; GB:X53959; NID:98614; PIDN:CAA37910.1; PID:G
R;Rothberg, J.M.; Hartley, D.A.; Walther, Z.; Artavanis-Tsakonas, S.
Cell 55, 1047-1059, 1988
A;Title: slit: An EGF-homologous locus of D. melanogaster involved in the development of
A;Reference number: A31640; MUID: 89077533; PMID: 3144436
A;Accession: A31640
A;Molecule type: DNA
A;Residues: 881-1182, 'G', 1185-1404, 'GT', 1463-1464, 'YHA', 'RO2'
A;Cross-references: UNIPARC:UPI000016BD7A; GB:M23543; NID:9340939; PID:G514357
C;Genetics:
A;Gene: FlyBase:slit
A;Cross-references: FlyBase:FBgn0003425
A;Introns: 1351/3
C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein
C;Keywords: alternative splicing; growth factor
F;66-91/Domain: proteoglycan amino-terminal homology <PAH1>
F;101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;197-220/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;228-272/Domain: proteoglycan carboxyl-terminal homology <PCS1>
F;288-313/Domain: proteoglycan amino-terminal homology <PAH2>
F;323-346/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;347-370/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;395-418/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F;419-442/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>
F;450-494/Domain: proteoglycan carboxyl-terminal homology <PCS2>
F;512-537/Domain: proteoglycan amino-terminal homology <PAH3>
F;547-571/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>
F;572-595/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>
F;596-619/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>
F;620-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>
F;651-695/Domain: proteoglycan carboxyl-terminal homology <PCS3>
F;708-733/Domain: proteoglycan amino-terminal homology <PAH4>
F;743-766/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>
F;767-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR16>
F;791-814/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR17>
F;815-838/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR18>
F;846-890/Domain: proteoglycan carboxyl-terminal homology <PCS4>
F;1028-1061/Domain: EGF homology <EGF>
F;1068-1099/Domain: EGF homology <EGF2>
F;1115-1148/Domain: EGF homology <EGF1>

Query Match 8.1%; Score 255.5; DB 2; Length 1480;
Best Local Similarity 21.4%; Pred. No. 4e-07;
Matches 105; Conservative 52; Mismatches 168; Indels 165; Gaps 14;

QY 199 LSLQALPG-----DLSGLFPLRLLAARPNFNCVCLSPWFPGWVRES 241
 DB 235 NSLSAPEGWASLQGNWMDRGDFDSG-----NFWICDQNSLDLYRWLQAQ 282
 QY 242 HVTLASPEETCHFFPKNAGRLLL 265
 DB 283 KDKMFSDNTRCAGPEAVKGTLL 306

RESULT 13
 A60164
 Platelet membrane glycoprotein V precursor - human
 C:Species: Homo sapiens (man)
 C>Date: 12-Jan-1993 #sequence revision 24-Feb-1994 #text change 09-Jul-2004
 C:Accession: A60164; A35483; B35483; C35483; A60432; A47507; S34329
 R:Lanza, F.; Morales, M.; de La Salle, C.; Cazenave, J.P.; Clemetson, K.J.; Shimomura, T.
 J. Biol. Chem. 268, 20801-20807, 1993
 A:Title: Cloning and characterization of the gene encoding the human platelet glycoprotein V
 A:Reference number: A48030; MUID:94012616; PMID:8407908
 A:Accession: A48030
 A:Molecule type: DNA
 A:Residues: 1-560 <LA2>
 A:Cross-references: UNIPROT:P40197; UNIPARC:UPI000004B117; EMBL:Z23091; NID:g312501; PID:RShimomura, T.; Fujimura, K.; Maehama, S.; Takemoto, M.; Oda, K.; Fujimoto, T.; Oyama, Blood 75, 2349-2356, 1990
 A:Title: Rapid purification and characterization of human platelet glycoprotein V: the a
 A:Reference number: A60164; MUID:90275263; PMID:2350580
 A:Accession: A60164
 A:Molecule type: protein
 A:Residues: 365-384, 'X', 386-390, 'X', 392-395, 'X', 397,188-208, 'I', 210,27-50, 'X', 52-53,174-
 'XX',108, 'T', 61-72, 'TK', 75-77, 'V', 56-57, 'G', 479-487, 'X', 489-498, 'X', 500, 'X', 502-503, 'X',
 A:Cross-references: UNIPARC:UPI000017C2F6; UNIPARC:UPI000017C2F7; UNIPARC:UPI000017C2F8;
 2FD; UNIPARC:UPI000017C2F9; UNIPARC:UPI000017C2FF; UNIPARC:UPI000017C300; UNIPARC:UPI000
 R:Roth, G.J.; Church, T.A.; McMullen, B.A.; Williams, S.A.
 Biochem. Biophys. Res. Commun. 170, 153-161, 1990
 A:Title: Human platelet glycoprotein V: a surface leucine-rich glycoprotein related to a
 A:Reference number: A35483; MUID:90321220; PMID:2372284
 A:Accession: A35483
 A:Molecule type: protein
 A:Residues: 145-166, 'I', 168-169, 'X', 171-172 <ROT>
 A:Cross-references: UNIPARC:UPI000017C303
 A:Note: this proteolytic fragment was designated peptide M392
 A:Accession: B35483
 A:Molecule type: protein
 A:Residues: 121-129, 'W', 131-135,466-468, 'X', 470 <RO2>
 A:Cross-references: UNIPARC:UPI000017C304; UNIPARC:UPI000017C305
 A:Note: this material was designated peptide M393 but may contain two peptides
 A:Accession: C35483
 A:Molecule type: protein
 A:Residues: 252-266, 'H', 268-272, 'X', 274-279, 'I', 281-284, 'I', 286 <RO3>
 A:Cross-references: UNIPARC:UPI000017C306
 A:Note: this proteolytic fragment was designated peptide M401
 R:Zafar, R.S.; Walz, D.A.
 Thromb. Res. 53, 31-44, 1989
 A:Title: Platelet membrane glycoprotein V: characterization of the thrombin-sensitive gl
 A:Reference number: A60432; MUID:89162331; PMID:2922700
 A:Accession: A60432
 A:Molecule type: protein
 A:Residues: 477-478, 'FX', 481-485, 'E', 487, 'V', 489-492, 'NQ', 495, 'E', 497-498 <ZAF>
 A:Cross-references: UNIPARC:UPI000017C307
 R:Hickey, M.J.; Hagen, F.S.; Yagi, M.; Roth, G.J.
 Proc. Natl. Acad. Sci. U.S.A. 90, 8327-8331, 1993
 A:Title: Human platelet glycoprotein V: characterization of the polypeptide and the rela
 A:Reference number: A47507; MUID:93391348; PMID:7690959
 A:Accession: A47507
 A:Status: preliminary; translated from GB/EMBL/DBSJ
 A:Molecule type: mRNA
 A:Residues: 1-560 <RES>
 A:Cross-references: UNIPARC:UPI000004B117; GB:L11238; NID:g388759; PIDN:AAA03069.1; PID:
 C:Comment: This platelet membrane protein is a substrate for thrombin.
 C:Comment: The amino end of the intact protein is blocked.
 C:Comment: This protein is absent in Bernard-Soulier syndrome.
 C:Genetics:

A:Gene: GDB:GPS
 A:Cross-references: GDB:230236; OMIM:173511
 A:Map position: 5pter-5qter
 C:Keywords: blocked amino end; glycoprotein; platelet; tandem repeat; transmembrane prot

Query Match 7.7%; Score 240; DB 2; Length 560;
 Best Local Similarity 27.2%; Pred. NO. 1e-06;
 Matches 109; Conservative 28; Mismatches 111; Indels 152; Gaps 14;

QY 57 LYVFENGITMLDASSFAGLPGQLLDLSQNI-----ASL--RLPRLLLLDLSHNSILLALE 110
 DB 127 LFLDHNAURGIDQNMFKLVNLQELALNQNDLFLPASLTNLENLKLLDLSGNNLTHLP 186
 QY 111 PGILDT-ANVEALRLAGLQQLDDEGL-----FSRLRNLDH 145
 DB 187 KGLLGAQAKLERLLLSHNSRLVSLDGLNSLSLGAUTLOFHRNHIRSIAPGAFDLPLNLS 246
 QY 146 LDVS-----DNQLERVPPVIRG----- 162
 DB 247 LTLSRNLAFPLSALFLSHNLTLLTLFENPLAELPGVLFGBMGGLQBLWLNRTQLRTLP 306
 QY 163 ---LRGLTELRAGNT---RLAQLRPEDLAGLAALQELDV----- 196
 DB 307 AAAPFNLSRLRYLGVTLSPRLSALPQGAFOGLGELQVLALHNSNGLTALPDGLLRGLGKLR 366
 QY 197 -----SNLS-----LQALPGDLSGLFPLRLLAARPNFNCV 228
 DB 367 QVSLRRNLRALPRALFNLSLSVSQLDHNOLETLPDGVFGALPRLTEVLLGHNSWRCD 426
 QY 229 CPLSWFGPWVRESHVTLASPEE-TRCHFPFPKNAGRLLELDYADFGCPATTTTATVPTTR 287
 DB 427 CGLGFLGLWLRQ-HLGLVGSEPPRCAGPGAGHGLPLWALPGDAECFG-----PRGP 478
 QY 288 PWTREPTALSLSLAPTWLSPTAPATEAPSPSTAPPTVGP 327
 DB 479 P--PRPAADSS-----EAPVHPALAPNSSEP 503

RESULT 14
 JC7763
 neuronal leucine-rich repeat protein-3 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
 C:Accession: JC7763
 R:Fukamachi, K.; Matsuoka, Y.; Kitanaka, C.; Kuchino, Y.; Tsuda, H.
 Biochem. Biophys. Res. Commun. 287, 257-263, 2001
 A:Title: Rat neuronal leucine-rich repeat protein-3: Cloning and regulation of the gene
 A:Reference number: JC7763; PMID:11549284
 A:Contents: Fibrosarcoma cells
 A:Accession: JC7763
 A:Molecule type: mRNA
 A:Residues: 1-707 <FUK>
 A:Cross-references: UNIPROT:Q9BSY6; UNIPARC:UPI000004F0F2; GB:AF291437
 C:Comment: This protein, a new member of the neuronal leucine-rich repeat protein family
 in protein-protein interaction and functions as a cell adhesion molecule or soluble liga
 C:Genetics:
 A:Gene: nlrr-3
 C:Keywords: cell adhesion

Query Match 7.6%; Score 237; DB 2; Length 707;
 Best Local Similarity 20.7%; Pred. NO. 2e-06;
 Matches 127; Conservative 80; Mismatches 22; Indels 186; Gaps 22;

QY 6 PLLPLLLLLLALGPGVQG-----CPSCQCS-----QPQVFTCARQGTTPV 47
 DB 5 PLQIHVLGLAITALVQAGDKKVCQPCQCTCIRPFWFTPRSIYMEASTVDCNDLGLNFP 64
 QY 48 RDVDPDVTGLVVFENGITMLDASSFAGLP-GLQLLDLSQNIASI----- 91
 DB 65 ARLPADYQIILLQNNIARIHSHT--DPFVNLTGLDLSQNNLSSTVINNVQMSQLLSVY 122
 QY 92 -----RLPRLLLLDLS-----HNSLLALSPGIL----- 114

Db 123 LEENKLTPEKCLYGLSNLQELVYVNHNLSSAISPGAFVGLHNLRLHLNSNRLQWINSK 182
QY 115 ---DTANVEALRL-----AGLGLQQLDEGLFSRLNHLHLD 147
Db 183 WFEALPNLEILMGDNPIILRIKDMNFQPLKLSLVIAGINLTVEPDDALVGLNLEGIS 242
QY 148 VSDNOLERV-----PVIIRGLRG----- 165
Db 243 FYDNRINKVPQVALQKAVNLKFDLKNKPNIRRGDFSNMHLKELGINNPELVISIDS 302
QY 166 -----LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLOAL-PGDLISGLFPRLR 216
Db 303 LAVDNLPDLRKIEATNNPRLSYIHPNAPFLPKLSLMLNSALSALYHGTTIESL-PNLK 361
QY 217 LLAARARNPNCVPLSWFGPWREHSHVTLASPEETRCHPPKKNAGRLLELDYADFGCPA 276
Db 362 EISIHSPNTRCDVIRWIN--NPKTNIRFMEPDSLFCVDPPEFGQNVQVHFRDM---- 415
QY 277 TTTTATVPTTRPVVREPTALSSSL---APTMLSPTAPATEAPSPSTAPPTVGPVPQPD 333
Db 416 -----MEICLPLI-APESFPSILDVEADSVVSLHCRATAEPQ-----PEIYWIITPSGKR 463
QY 334 CPPSTCLNGGTCHL-GTRHHLACLCEPGETGLY---CESQMGGTRPSPTPTVTPRPPR-- 387
Db 464 LLPNTLREKFVYHSEGTLDIRGTPKEG--GLYTCTATNLVGLADLSIMIKVGGFVPQDN 521
QY 388 ---SLTLGIEPVPSTLRVGLQRYLOGSSVOLRSRLRTVRLNSGPKRLVTLRLPASLAEY 445
Db 522 NGSLNIKIRDIRANSVLVS---WKANSKILKSVMKVFVKTEDSQAAQSARIPSDVKVY 578
QY 446 TVTQLRPNATYSVCV 460
Db 579 NLTHLKSTPEYKICI 593

RESULT 15
T42626
secreted leucine-rich repeat-containing protein SLIT2 - mouse (fragment)
N:Alternate names: neurogenic extracellular slit protein
C:Species: Mus musculus (house mouse)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T42626
R:Holmes, G.P.; Negus, K.; Raman, S.; Algar, E.; Yamada, T.; Little, M.H.
Mech. Dev. 79, 57-72, 1998
A:Title: Distinct but overlapping expression patterns of two vertebrate slit homologs in
A:Reference number: Z22177; MUID:99279238; PMID:10349621
A:Accession: T42626
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1025 <HOL>
A:Cross-references: UNIPROT:Q9R1B9; UNIPARC:UPI00000E8104; EMBL:AF074960; NID:g4151258;
C:Gene: Slit2
C:Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein

Query Match 7.4%; Score 231; DB 2; Length 1025;
Best Local Similarity 24.0%; Pred. No. 6.9e-06;
Matches 89; Conservative 32; Mismatches 122; Indels 128; Gaps 13;

QY 24 CPSCGQCSPQVFTARQTTVPRDVPDVTGLYVFENGITMLDASSFAGLGLQLDL 83
Db 223 CPSECTCLD-TVRCGSKGLKVLPGIPKDVTELYLDGNOFTLV-PKELSNYKHLTLIDL 280
QY 84 SQNQIASL-----RLPRLLLDLGSHNSLLALEPGILDPTANVEALRLAGLGLQQLDEGLIF 137
Db 281 SNNRISLNSNOXFSNNMTQLTLILSYNRLRCIPPTFD-----GLKSL----- 323
QY 138 SPLRLNHLDVDNQLRVPVPIRGRLRLAGNTRIAQLRPEDLAGLAALQELDVS 197
Db 324 -RLLSLHGNDIS-----VVP----- 337
QY 198 NLSLQALPGDLGLFRLRLAAARNPNCVPLSWFGPWREHSHVTLASPEETRCHPPP 257

Db 338 ----EGAFNDLSA-----LSHLAIGANPLYCDNQMLSDWKSEY---KEPGIARCAGPG 386
QY 258 KNAGRLILLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLAPTWLSPATAPATEAPSP 317
Db 387 EMADKLLLTTPSKKFTCQ-----GPMDITIQAACNPNCLSN 421
QY 318 PSTAPPTVGPVP-----QPQDCP-----PSTCLNGGTCHL--GTRHHLACL 356
Db 422 PKNDGTNNNDPVDFYRCTCPYGFKGQCDVPIHACISNPKCHGSGTCHLKEGENAGFWCT 481
QY 357 CPEGFTGLYCE 367
Db 482 CADGFEENCE 492

Search completed: February 7, 2006, 16:18:13
Job time : 58 secs

GenCore version 5.1.7
 Copyright (c) 1993 - 2006 Bioceleration Ltd.
 OM protein - protein search, using sw model
 Run on: February 7, 2006, 16:12:51 ; Search time 251 Seconds
 (without alignments)
 1680.900 Million cell updates/sec

Title: US-10-677-669-69
 Perfect score: 3135
 Sequence: 1 MCSRVELLLPLLLALLALPG.....PLMGPPGGLQSLHAKPYI 598

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Liefting first 1500 summaries

Database : Uniprot_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3135	100.0	598	2	Q6UXL5_HUMAN
2	3083.5	98.4	673	2	Q6UXL4_HUMAN
3	3078.5	98.2	673	2	Q6ENK4_HUMAN
4	2697.5	86.0	601	2	Q96CX1_HUMAN
5	2491	79.5	673	2	Q8BJU0_MOUSE
6	2490	79.4	673	2	Q8RZG5_MOUSE
7	2484	79.2	673	2	Q9CZT5_MOUSE
8	1213.5	38.7	661	2	Q6DF55_XENTR
9	927.5	29.6	643	2	Q503G2_BRARE
10	914.5	29.2	962	2	Q4S068_TETNG
11	368.5	11.8	513	2	Q50LG9_HUMAN
12	359.5	11.5	635	1	LRFN4_HUMAN
13	351	11.2	636	1	LRFN4_MOUSE
14	341	10.9	660	2	Q8BLU0_MOUSE
15	339	10.8	521	2	Q8BHAL_MOUSE
16	338	10.8	655	2	Q4SGV9_TETNG
17	333	10.6	858	2	Q5TYT7_BRARE
18	332	10.6	637	2	Q6A073_MOUSE
19	331.5	10.6	622	2	Q59GV4_HUMAN
20	330	10.5	653	1	LRRC4_HUMAN
21	329.5	10.5	648	2	Q6DDY0_XENLA
22	325.5	10.4	570	2	Q70AK2_XENLA
23	324	10.3	626	1	LRFN3_MOUSE
24	324	10.3	626	2	Q505E2_MOUSE
25	323	10.3	732	2	Q4RPB8_TETNG
26	322.5	10.3	682	2	Q6DJD2_XENLA
27	322.5	10.3	811	2	Q7L0X0_HUMAN
28	322.5	10.3	887	2	Q75139_HUMAN
29	322	10.3	605	1	ALS_PAPHA
30	321	10.2	628	1	LRFN3_HUMAN
31	321	10.2	762	2	Q5JYV13_HUMAN

32	320	10.2	660	1	FLRT2_HUMAN
33	320	10.2	674	2	Q6RKD8_MOUSE
34	319	10.2	602	2	Q58CS0_BOVIN
35	318.5	10.2	652	1	LRRC4_MOUSE
36	317.5	10.1	778	2	Q6NUI6_HUMAN
37	312.5	10.0	648	2	Q70AK3_XENLA
38	312.5	10.0	935	2	Q4SBT7_TETNG
39	311.5	9.9	420	2	Q7M6Z0_MOUSE
40	310.5	9.9	420	2	Q8OWD1_RAT
41	310.5	9.9	646	1	FLRT1_HUMAN
42	308	9.8	627	2	Q8NC95_HUMAN
43	308	9.8	649	1	FLRT3_HUMAN
44	308	9.8	649	2	Q542Z9_HUMAN
45	307.5	9.8	626	2	Q4TEM8_TETNG
46	307.5	9.8	674	2	Q8WVA2_HUMAN
47	307	9.8	637	2	Q68F21_XENLA
48	307	9.8	639	2	Q5R6T0_PONPY
49	306.5	9.8	730	2	Q6PHP6_MOUSE
50	305.5	9.7	730	2	Q6US92_MOUSE
51	303.5	9.7	692	2	Q4G0S0_HUMAN
52	302.5	9.6	420	2	Q6X813_HUMAN
53	302.5	9.6	420	2	Q86UN3_HUMAN
54	302.5	9.6	618	2	Q4SHD7_TETNG
55	302	9.6	605	1	ALS_HUMAN
56	302	9.6	605	2	Q8TAY0_HUMAN
57	299.5	9.6	677	2	Q28256_CANFA
58	298.5	9.5	649	2	Q8BGT1_MOUSE
59	298.5	9.5	663	2	Q6ZPQ1_MOUSE
60	295.5	9.4	640	1	NGLI1_MOUSE
61	295.5	9.4	640	2	Q505E5_MOUSE
62	294.5	9.4	640	2	Q50317_BRARE
63	293.5	9.4	809	2	Q9DBY4_MOUSE
64	292.5	9.3	640	1	NGLI1_HUMAN
65	292.5	9.3	837	2	Q80TV0_MOUSE
66	288.5	9.2	372	2	Q7F2W3_BRARE
67	288.5	9.2	581	2	Q4SYI7_TETNG
68	288.5	9.2	640	2	Q4JIW0_HUMAN
69	287.5	9.2	428	2	Q4S4W6_TETNG
70	287.5	9.2	713	1	LRN5_HUMAN
71	286	9.1	650	2	Q4RQ15_TETNG
72	285	9.1	650	2	Q4JIV9_HUMAN
73	284.5	9.1	457	2	Q6WZD1_BRARE
74	284	9.1	782	2	Q5T0V4_HUMAN
75	283.5	9.0	603	2	Q70211_RAT
76	283	9.0	1515	2	Q9DE37_BRARE
77	282.5	9.0	745	2	Q6UXK2_HUMAN
78	282.5	9.0	785	2	Q9P263_HUMAN
79	282	9.0	626	1	GP1BA_HUMAN
80	281.5	9.0	603	1	ALS_RAT
81	281	9.0	738	2	Q90Z45_CHICK
82	280	8.9	633	2	Q4SR95_TETNG
83	279.5	8.9	619	2	Q570Z9_MOUSE
84	278.5	8.9	603	1	ALS_MOUSE
85	278.5	8.9	603	2	Q791Q5_MOUSE
86	278.5	8.9	687	2	Q79JL0_MOUSE
87	278	8.9	321	2	Q6E4K4_PETMA
88	278	8.9	1531	1	SLIT1_RAT
89	277	8.8	330	2	Q4G1K3_EPTBU
90	276	8.8	1071	2	Q4RTI6_TETNG
91	276	8.8	1531	1	SLIT1_MOUSE
92	276	8.8	2623	2	Q6WRI0_HUMAN
93	273.5	8.7	593	2	Q6UY18_HUMAN
94	273.5	8.7	1504	1	SLIT1_DROME
95	273	8.7	745	2	Q5RKR3_MOUSE
96	273	8.7	785	2	Q6ZPQ3_MOUSE
97	271.5	8.7	342	2	Q91XL1_MOUSE
98	271.5	8.7	1312	2	Q61PF0_CAEBR
99	271	8.6	473	1	RTN4R_HUMAN
100	271	8.6	473	1	RTN4R_MACFA
101	270.5	8.6	541	2	Q6PK41_HUMAN
102	270	8.6	478	2	Q6WZD2_BRARE
103	270	8.6	1461	2	Q5VW18_HUMAN
104	270	8.6	1534	1	SLIT1_HUMAN

043155	homo sapien
Q6rkd8	mus musculus
Q58cso	bos taurus
Q99ph1	mus musculus
Q6nu16	homo sapien
Q70ak3	xenopus lae
Q4sb7	tetradon n
Q7m6z0	mus musculus
Q80wd1	rattus norv
Q9nzul	homo sapien
Q8nc95	homo sapien
Q9nzuo	homo sapien
Q542z9	homo sapien
Q4tmb8	tetradon n
Q8wva2	homo sapien
Q68f21	xenopus lae
Q5r6t0	pongo pygma
Q6php6	mus musculus
Q6us92	mus musculus
Q4g0s0	homo sapien
Q6x813	homo sapien
Q86un3	homo sapien
Q4shd7	tetradon n
P35958	homo sapien
Q8t5y0	homo sapien
Q28256	canis famil
Q8bgt1	mus musculus
Q6zpq1	mus musculus
Q8c0j1	mus musculus
Q505e5	mus musculus
Q50317	brachydanio
Q9dby4	m mus muscu
Q9hcj2	homo sapien
Q80tv0	mus musculus
Q7taw3	brachydanio
Q4syi7	tetradon n
Q4jiw0	homo sapien
Q4s4w6	tetradon n
Q75325	homo sapien
Q4rq15	tetradon n
Q4jiv9	homo sapien
Q6wzd1	brachydanio
Q5t0v4	homo sapien
Q70211	rattus norv
Q9de37	brachydanio
Q6uxk2	homo sapien
Q9p263	homo sapien
P07359	homo sapien
P35959	rattus norv
Q90z45	gallus gall
Q4sr95	tetradon n
Q570z9	mus musculus
P70389	mus musculus
Q791q5	mus musculus
Q9jil0	mus musculus
Q6e4k4	petromyzon
Q88279	rattus norv
Q4g1k3	eptatretus
Q4rti6	tetradon n
Q80tr4	mus musculus
Q6wri0	homo sapien
Q6uy18	homo sapien
P24014	drosophila
Q5rkr3	mus musculus
Q6zpq3	mus musculus
Q91xl1	mus musculus
Q61pf0	caenorhabdi
Q9bzr6	homo sapien
Q9n0e3	macaca fasc
Q6pk41	homo sapien
Q6wzd2	brachydanio
Q5vw18	homo sapien
Q75093	homo sapien

105	270	8.6	1534	2	Q5VW17_HUMAN	Q5VW17 homo sapien	178	242.5	7.7	545	1	CPN2_HUMAN	P22792 homo sapien
106	268.5	8.6	409	2	Q5T0V2_HUMAN	Q5T0V2 homo sapien	179	242.5	7.7	718	2	Q6PC4_XENLA	Q6pc4 xenopus lae
107	268	8.5	417	2	Q6E4J7_PETMA	Q6e4j7 petromyzon	180	242	7.7	380	2	Q5T0V3_HUMAN	Q5T0v3 homo sapien
108	267.5	8.5	1512	2	Q9DE36_BRARE	Q9de36 brachydanio	181	242	7.7	652	2	Q7PVZ3_ANOGA	Q7pvz3 anopheles g
109	266.5	8.5	1529	2	Q7ZX12_XENLA	Q7zx12 xenopus lae	182	241.5	7.7	272	2	Q4KP12_LAMAP	Q4kp12 lampetra ap
110	266	8.5	460	2	Q61PL6_HUMAN	Q61pl6 homo sapien	183	241.5	7.7	311	2	Q6E4L3_PETMA	Q6e4l3 petromyzon
111	266	8.5	734	2	Q3S930_MOUSE	Q3s930 mus musculu	184	240	7.7	560	1	GPV_HUMAN	P40197 homo sapien
112	265.5	8.5	1044	2	Q5ISR9_MACFA	Q5isr9 macaca fasc	185	239.5	7.6	370	2	Q8BGX3_MOUSE	Q8bgx3 m mus muscu
113	265	8.4	298	2	Q4G1L7_EPTBU	Q4g1l7 eptatretus	186	239.5	7.6	786	2	Q5TU01_ANOGA	Q5tu01 anopheles g
114	265	8.5	734	2	Q5XK47_MOUSE	Q5xk47 mus musculu	187	239.5	7.6	1256	2	Q7QCT2_ANOGA	Q7qct2 anopheles g
115	264.5	8.4	420	1	TPBG_HUMAN	Q13641 homo sapien	188	238	7.6	323	2	Q4KP13_9PETR	Q4kp13 ichtthyomyzo
116	264	8.4	332	2	Q5VSG2_HUMAN	Q5vsg2 homo sapien	189	238	7.6	453	2	Q86XV1_HUMAN	Q86xv1 homo sapien
117	264	8.4	354	2	Q4G1L1_EPTBU	Q4g1l1 eptatretus	190	238	7.6	544	2	Q8UV23_9PERC	Q8uv23 sphoeroides
118	263	8.4	332	2	Q5IOE1_RAT	Q5ioe1 rattus norv	191	237.5	7.6	391	2	Q9D3K0_MOUSE	Q9d3k0 m mus muscu
119	263	8.4	1253	2	Q4T0S1_TETNG	Q4t0s1 tetraodon n	192	237.5	7.6	1174	2	Q4S4C0_TETNG	Q4s4c0 tetraodon n
120	262	8.4	346	2	Q4G1L9_EPTBU	Q4g1l9 eptatretus	193	237	7.6	289	2	Q4KP06_LAMAP	Q4kp06 lampetra ap
121	261.5	8.3	347	1	A2GL_HUMAN	P03750 homo sapien	194	237	7.6	370	2	Q8N967_HUMAN	Q8n967 homo sapien
122	261	8.3	1523	1	SLIT3_RAT	Q88280 rattus norv	195	237	7.6	578	1	LRC15_RAT	Q8r5m3 rattus norv
123	258	8.2	321	2	Q6E4D1_PETMA	Q6e4d1 petromyzon	196	237	7.6	707	2	Q9ESY6_RAT	Q9esy6 rattus norv
124	258	8.2	1223	1	SLIT3_HUMAN	Q75094 homo sapien	197	237	7.6	1046	2	Q7FZJ7_ANOGA	Q7fzj7 anopheles g
125	257.5	8.2	324	2	Q4S3K9_TETNG	Q4s3k9 tetraodon n	198	236.5	7.5	461	2	Q4SA12_TETNG	Q4sal2 tetraodon n
126	257.5	8.2	501	2	Q4SZC5_TETNG	Q4szc5 tetraodon n	199	236.5	7.5	715	2	Q4RY04_TETNG	Q4ry04 tetraodon n
127	257	8.2	473	1	RTN4R_RAT	Q9m75 rattus norv	200	236	7.5	707	2	Q8CBC6_MOUSE	Q8cbc6 mus musculu
128	257	8.2	739	2	Q8BKM5_MOUSE	Q8bkm5 mus musculu	201	236	7.5	718	2	Q6P627_XENLA	Q6p627 xenopus lae
129	256.5	8.2	342	2	Q4SGG5_TETNG	Q4sgg5 tetraodon n	202	235.5	7.5	296	2	Q4G1H6_EPTST	Q4glh6 eptatretus
130	255.5	8.1	1095	2	Q90XG4_CHICK	Q90xg4 gallus gall	203	235.5	7.5	579	1	LRC15_MOUSE	Q80x72 mus musculu
131	254	8.1	528	2	Q8N644_HUMAN	Q8n644 homo sapien	204	235	7.5	574	2	Q4RRK5_TETNG	Q4rrk5 tetraodon n
132	254	8.1	1523	1	SLIT3_MOUSE	Q9wvb4 mus musculu	205	234.5	7.5	488	2	Q4RK86_TETNG	Q4rk86 tetraodon n
133	254	8.1	1523	2	Q5SS56_MOUSE	Q5ss56 mus musculu	206	234	7.5	707	2	P97860_MOUSE	P97860 mus musculu
134	253.5	8.1	347	2	Q68CK4_HUMAN	Q68ck4 homo sapien	207	233.5	7.4	298	2	Q6E4J4_PETMA	Q6e4j4 petromyzon
135	253.5	8.1	589	2	Q6GQU6_MOUSE	Q6gqu6 mus musculu	208	233.5	7.4	545	2	Q5R534_PONPY	Q5r534 pongo pygma
136	253.5	8.1	1410	2	Q20Z04_CABEL	Q20z04 caenorhabdi	209	233	7.4	1316	2	Q9VQ25_DROME	Q9vq25 drosophila
137	253	8.1	426	1	TPBG_MOUSE	Q08742 mus musculu	210	232	7.4	487	2	Q4SA13_TETNG	Q4sal3 tetraodon n
138	253	8.1	567	1	GPV_MOUSE	Q08742 mus musculu	211	231.5	7.4	283	2	Q4G1H4_EPTST	Q4glh4 eptatretus
139	252	8.0	311	2	Q6E4L1_PETMA	Q6e4l1 petromyzon	212	231.5	7.4	840	1	SLIK6_MOUSE	Q8c110 mus musculu
140	252	8.0	426	1	TPBG_RAT	Q5pgv5 rattus norv	213	231	7.4	294	2	Q5VT99_HUMAN	Q5vt99 homo sapien
141	252	8.0	567	2	Q9QZU3_MOUSE	Q9qzu3 mus musculu	214	231	7.4	547	1	CPN2_MOUSE	Q9dbb9 mus musculu
142	251	8.0	473	1	RTN4R_MOUSE	Q99p18 mus musculu	215	231	7.4	619	2	Q7QBW2_ANOGA	Q7qbw2 anopheles g
143	251	8.0	542	2	Q9N4G6_CABEL	Q9n4g6 caenorhabdi	216	231	7.4	707	2	Q642B4_RAT	Q642e4 rattus norv
144	251	8.0	622	2	Q6ZW15_HUMAN	Q6zw15 homo sapien	217	231	7.4	787	2	Q4SW26_TETNG	Q4sw26 tetraodon n
145	251	8.0	622	2	Q72Q07_HUMAN	Q72q07 homo sapien	218	230.5	7.4	687	2	Q4SCX3_TETNG	Q4scx3 tetraodon n
146	251	8.0	1021	2	Q9V430_DROME	Q9v430 drosophila	219	230	7.3	332	2	Q8QFN6_ELAQU	Q8qfn6 elaphe quad
147	250	8.0	412	2	Q4RRU8_TETNG	Q4rru8 tetraodon n	220	230	7.3	332	2	Q8QFN7_ELAQU	Q8qfn7 elaphe quad
148	249.5	8.0	789	1	LRFN2_HUMAN	Q9ulh4 homo sapien	221	230	7.3	872	2	Q4SZ04_TETNG	Q4sz04 tetraodon n
149	249.5	8.0	789	1	LRFN2_MACFA	Q9be71 macaca fasc	222	230	7.3	1229	2	Q4T7S0_TETNG	Q4t7s0 tetraodon n
150	249.5	8.0	297	2	Q6WRH9_RAT	Q6wrh9 rattus norv	223	229.5	7.3	828	2	Q8C8T7_MOUSE	Q8c8t7 mus musculu
151	248.5	7.9	420	1	TPBG_MACFA	Q4r8y9 macaca fasc	224	229	7.3	581	1	LRC15_HUMAN	Q8tf66 homo sapien
152	248	7.9	481	1	NYX_HUMAN	Q9gzus homo sapien	225	228.5	7.3	294	2	Q6E4L6_PETMA	Q6e4l6 petromyzon
153	248	7.9	481	2	Q5H983_HUMAN	Q5h983 homo sapien	226	228.5	7.3	341	2	Q6ZSA7_HUMAN	Q6zsa7 homo sapien
154	247.5	7.9	305	2	Q4G1L3_EPTBU	Q4g1l3 eptatretus	227	228.5	7.3	342	2	Q4RRU5_TETNG	Q4rru5 tetraodon n
155	247.5	7.9	1521	1	SLIT2_MOUSE	Q9rlb9 mus musculu	228	228	7.3	310	2	Q4RRQ4_TETNG	Q4rrq4 tetraodon n
156	247.5	7.9	1529	1	SLIT2_HUMAN	Q94813 homo sapien	229	228	7.3	838	2	Q4SPF9_TETNG	Q4spp9 tetraodon n
157	247.5	7.9	1530	2	Q90WZ3_XENLA	Q90wz3 xenopus lae	230	227.5	7.3	356	2	Q8BXQ3_MOUSE	Q8bxq3 m mus muscu
158	247	7.9	794	2	Q4SK16_TETNG	Q4sk16 tetraodon n	231	227	7.2	326	2	Q4KLL3_RAT	Q4kll3 rattus norv
159	246	7.8	308	2	Q4G1L3_EPTST	Q4g1l3 eptatretus	232	227	7.2	783	2	Q90XG2_CHICK	Q90xg2 gallus gall
160	245.5	7.8	334	2	Q91W20_MOUSE	Q91w20 mus musculu	233	227	7.2	950	2	Q90Z44_CHICK	Q90z44 gallus gall
161	245.5	7.8	544	2	Q61X58_CABBR	Q61x58 caenorhabdi	234	226.5	7.2	283	2	Q4G1L1_EPTST	Q4gl11 eptatretus
162	245	7.8	306	2	Q4G1K6_EPTST	Q4g1k6 eptatretus	235	226.5	7.2	298	2	Q4KP15_9PETR	Q4kp15 ichtthyomyzo
163	245	7.8	321	2	Q6E4J9_PETMA	Q6e4j9 petromyzon	236	226.5	7.2	299	2	Q4G1I9_EPTST	Q4g1i9 eptatretus
164	245	7.8	708	2	Q81YQ6_HUMAN	Q81yq6 homo sapien	237	226.5	7.2	557	1	LG11_HUMAN	Q95970 homo sapien
165	245	7.8	708	2	Q5B482_PONPY	Q5b482 pongo pygma	238	226.5	7.2	719	1	LFPN5_HUMAN	Q96ni6 homo sapien
166	244.5	7.8	411	2	Q4S6L6_TETNG	Q4s6l6 tetraodon n	239	226	7.2	321	1	Q4KP16_9PETR	Q4kp16 ichtthyomyzo
167	244.5	7.8	718	2	Q73675_XENLA	Q73675 xenopus lae	240	226	7.2	364	2	Q4SQ63_TETNG	Q4sq63 tetraodon n
168	244.5	7.8	766	1	SLIT2_RAT	Q9wvc1 rattus norv	241	225.5	7.2	210	2	Q4SCF1_TETNG	Q4scf1 tetraodon n
169	244.5	7.8	788	1	LRFN2_MOUSE	Q80tg9 mus musculu	242	225.5	7.2	298	2	Q6E4J3_PETMA	Q6e4j3 petromyzon
170	244.5	7.8	1593	2	Q5DTL5_MOUSE	Q5dtl5 mus musculu	243	223.5	7.1	283	2	Q4G1H8_EPTST	Q4glh8 eptatretus
171	244	7.8	458	2	Q6WZD3_BRARE	Q6wzd3 brachydanio	244	223.5	7.1	647	2	Q4S1N0_TETNG	Q4s1n0 tetraodon n
172	244	7.8	567	1	GPV_RAT	Q08770 rattus norv	245	223	7.1	349	2	Q6E4C8_PETMA	Q6e4c8 petromyzon
173	244	7.8	708	2	Q9H3W5_HUMAN	Q9h3w5 homo sapien	246	223	7.1	289	2	Q4SH52_TETNG	Q4sh52 tetraodon n
174	243.5	7.8	476	1	NYX_MOUSE	P83503 mus musculu	247	222.5	7.1	413	2	Q642I5_MOUSE	Q642i5 mus musculu
175	243	7.8	321	2	Q6E4L4_PETMA	Q6e4l4 petromyzon	248	222.5	7.1	557	1	LG11_RAT	Q8k4y5 rattus norv
176	243	7.8	708	2	Q619V8_HUMAN	Q619v8 homo sapien	249	222.5	7.1	557	2	Q5R945_PONPY	Q5r945 pongo pygma
177	242.5	7.7	388	2	Q6ZM54_BRARE	Q6zm54 brachydanio	250	222.5	7.1	557	2	Q5FWS7_RAT	Q5fw87 rattus norv

251	222.5	7.1	792	2	Q90243_CHICK	Q90243_gallus_gall	324	209	6.7	358	2	Q5SUV4_MOUSE	Q5SUV4_mus_musculus
252	222	7.1	269	2	Q6B410_PETMA	Q6E410_tetrazodon_n	325	209	6.7	391	1	Q4S8B7_TETNG	Q4S8B7_tetrazodon_n
253	222	7.1	348	2	Q9S5J8_MACFA	Q9E510_macaca_fasc	326	209	6.7	1091	1	LRIG1_MOUSE	LRIG1_mus_musculus
254	222	7.1	725	2	Q5PPU2_XENLA	Q5P202_xenopus_lae	327	208.5	6.7	350	2	Q5RH05_BRARE	Q5RH05_brachydanio
255	221.5	7.1	475	2	Q4T109_TETNG	Q4T109_tetrazodon_n	328	208.5	6.7	382	1	PRELP_HUMAN	PRELP_homo_sapien
256	221.5	7.1	557	1	LG11_MOUSE	Q9J1a1_mus_musculus	329	208.5	6.7	382	1	Q6FHG6_HUMAN	Q6FHG6_homo_sapien
257	221.5	7.1	719	1	LRFN5_MOUSE	Q8Bxa0_mus_musculus	330	208.5	6.7	382	2	Q6FG38_HUMAN	Q6FG38_homo_sapien
258	221.5	7.1	721	1	Q5DTH4_MOUSE	Q5Dth4_mus_musculus	331	208.5	6.7	445	2	Q8K0S5_MOUSE	Q8K0S5_m_reticulon
259	221	7.1	1093	1	LRIG1_HUMAN	Q964m1_homo_sapien	332	208.5	6.7	479	2	Q6X3Y5_BRARE	Q6X3Y5_brachydanio
260	220.5	7.0	306	2	Q6E4M1_PETMA	Q6E4m1_petromyzon	333	208.5	6.7	518	1	LRTH4_HUMAN	Q86vh4_homo_sapien
261	220.5	7.0	322	2	Q4BK04_LAMAP	Q4Kp04_lampetra_ap	334	208.5	6.7	518	2	Q4FZ98_HUMAN	Q4FZ98_homo_sapien
262	220.5	7.0	342	2	Q6B4K1_PETMA	Q6E4k1_petromyzon	335	208.5	6.7	519	2	Q4KMX1_HUMAN	Q4Kmx1_homo_sapien
263	220.5	7.0	342	2	Q4RW94_TETNG	Q4rw94_tetrazodon_n	336	208.5	6.7	537	1	LG14_HUMAN	Q8n135_homo_sapien
264	220.5	7.0	515	1	LRTH2_MOUSE	Q8Bga3_mus_musculus	337	208.5	6.7	590	2	Q9VKJ7_HUMAN	Q9uxj7_homo_sapien
265	220.5	7.0	515	1	LRTH2_MOUSE	Q8Bga3_mus_musculus	338	208	6.6	649	2	Q9VKJ22_DROME	Q9vKj22_drosophila
266	220.5	7.0	733	2	Q24250_DROME	Q24250_drosophila	339	207.5	6.6	180	2	Q6B4F0_PETMA	Q6E4f0_petromyzon
267	220.5	7.0	841	1	SLIK6_HUMAN	Q9H5y7_homo_sapien	340	207.5	6.6	330	2	Q4S074_TETNG	Q4S074_tetrazodon_n
268	220	7.0	582	1	LRTH3_MOUSE	Q8Bz81_mus_musculus	341	207.5	6.6	518	2	Q6ZT31_HUMAN	Q6Zt31_homo_sapien
269	220	7.0	582	2	Q8BZA0_MOUSE	Q8Bza0_mus_musculus	342	207.5	6.6	1329	1	GP124_MOUSE	Q91xv8_mus_musculus
270	220	7.0	603	2	Q4S27_TETNG	Q4s27_tetrazodon_n	343	207	6.6	313	2	Q5T9K5_HUMAN	Q5T9k5_homo_sapien
271	219.5	7.0	583	2	Q4SNQ0_TETNG	Q4snq0_tetrazodon_n	344	207	6.6	313	2	Q8N7C0_HUMAN	Q8N7c0_homo_sapien
272	219	7.0	334	2	Q6P7C4_RAT	Q6p7c4_rattus_norv	345	207	6.6	536	2	Q8P0D2_BRARE	Q8P0d2_brachydanio
273	218.5	7.0	359	2	Q6GTU0_HUMAN	Q6gtu0_homo_sapien	346	207	6.6	613	2	Q50L44_CHICK	Q50L44_gallus_gall
274	218.5	7.0	618	1	LRC21_MOUSE	Q8K099_mus_musculus	347	207	6.6	740	2	Q5JMW6_HUMAN	Q5jmw6_homo_sapien
275	217.5	6.9	288	2	Q8BR15_MOUSE	Q8br15_mus_musculus	348	207	6.6	4293	2	Q08852_MOUSE	Q08852_mus_musculus
276	217.5	6.9	615	2	Q4SL57_TETNG	Q4sl57_tetrazodon_n	349	206.5	6.6	270	2	Q6B4K6_PETMA	Q6E4k6_petromyzon
277	217.5	6.9	695	2	Q4T1Y8_TETNG	Q4t1y8_tetrazodon_n	350	206.5	6.6	274	2	Q6B4B9_PETMA	Q6E4b9_petromyzon
278	217.5	6.9	1335	2	Q61OC7_CABER	Q61oc7_caenorhabdi	351	206.5	6.6	274	2	Q6B4C1_PETMA	Q6E4c1_petromyzon
279	217	6.9	637	2	Q6DCV7_XENLA	Q6dcv7_xenopus_lae	352	206.5	6.6	327	2	Q6B4L2_PETMA	Q6E4l2_petromyzon
280	216	6.9	283	2	Q6E4C7_PETMA	Q6E4c7_petromyzon	353	206.5	6.6	327	2	Q5U4S7_XENLA	Q5U4s7_xenopus_lae
281	216	6.9	282	2	Q4G1I6_EPTST	Q4g1i6_eptatretus	354	206.5	6.6	423	2	Q8ND46_HUMAN	Q8nd46_homo_sapien
282	216	6.9	514	2	Q4VBX1_MOUSE	Q4vbx1_mus_musculus	355	206.5	6.6	614	2	Q9D1T0_MOUSE	Q9d1t0_mus_musculus
283	215.5	6.9	329	2	Q56NG5_CIOIN	Q56ng5_ciona_intes	356	206	6.6	353	2	Q9UJX9_HUMAN	Q9ujx9_homo_sapien
284	215.5	6.9	331	1	PLIB_AKBL	Q56ng5_ciona_intes	357	206	6.6	353	2	Q8UJX8_HUMAN	Q8uJx8_homo_sapien
285	215.5	6.9	612	2	Q4SKY9_TETNG	Q4sky9_agkistrodon_n	358	206	6.6	381	1	PRELP_BOVIN	Q8wnu8_bos_taurus
286	215.5	6.9	737	2	Q9VU51_DROME	Q9vu51_drosophila	359	206	6.6	428	2	Q14498_HUMAN	Q14498_anopheles_g
287	215	6.9	743	2	Q6P1M7_HUMAN	Q6p1m7_homo_sapien	360	206	6.6	539	2	Q5TPW2_ANOGA	Q5tpw2_anopheles_g
288	214.5	6.8	329	2	Q56NG6_CIOIN	Q56ng6_ciona_intes	361	206	6.6	606	2	Q8BZD4_MOUSE	Q8Bzd4_mus_musculus
289	214.5	6.8	441	2	Q86UN2_HUMAN	Q86un2_homo_sapien	362	206	6.6	606	2	Q8BLC0_MOUSE	Q8blc0_mus_musculus
290	214.5	6.8	716	1	LRN1_HUMAN	Q6uxk5_homo_sapien	363	206	6.6	738	2	Q5U1A7_DROME	Q5u1a7_drosophila
291	214.5	6.8	731	2	Q4T149_TETNG	Q4t149_tetrazodon_n	364	206	6.6	1054	1	LRIG2_MOUSE	Q52kr2_mus_musculus
292	214.5	6.8	1535	2	Q23991_DROME	Q23991_drosophila	365	206	6.6	1127	2	Q4TAT9_TETNG	Q4tat9_tetrazodon_n
293	214	6.8	295	2	Q6E4C9_PETMA	Q6E4c9_petromyzon	366	205.5	6.6	212	2	Q6B4H2_PETMA	Q6E4h2_petromyzon
294	214	6.8	516	1	LRTH2_HUMAN	Q43300_homo_sapien	367	205.5	6.6	479	2	Q6DH76_BRARE	Q6dh76_brachydanio
295	214	6.8	717	2	Q4SR34_TETNG	Q4sr34_tetrazodon_n	368	205.5	6.6	492	2	Q9SKT6_MOUSE	Q9skt6_mus_musculus
296	214	6.8	2828	2	Q9NR99_HUMAN	Q9nr99_homo_sapien	369	205.5	6.6	590	1	LRTH4_MOUSE	Q80x99_mus_musculus
297	213.5	6.8	238	2	Q6E4J5_PETMA	Q6E4j5_petromyzon	370	205	6.5	248	2	Q4G1K4_EPTST	Q4g1k4_eptatretus
298	213.5	6.8	273	2	Q4G1L2_EPTBU	Q4g1l2_eptatretus	371	205	6.5	256	2	Q4G1L6_EPTBU	Q4g1l6_eptatretus
299	213.5	6.8	359	1	CHAD_HUMAN	Q15335_homo_sapien	372	205	6.5	486	2	Q4RU74_TETNG	Q4ru74_tetrazodon_n
300	213.5	6.8	361	1	CHAD_BOVIN	Q27972_bos_taurus	373	205	6.5	614	2	Q5RDJ4_PONPY	Q5rdj4_pongo_pygma
301	213	6.8	438	2	Q7TO96_RAT	Q7tc96_rattus_norv	374	205	6.5	614	2	Q9N008_MACFA	Q9n008_macaca_fasc
302	213	6.8	716	1	LRN1_MOUSE	Q61809_mus_musculus	375	205	6.5	620	2	Q96FE5_HUMAN	Q96fe5_homo_sapien
303	212.5	6.8	604	2	Q4SHE8_TETNG	Q4she8_tetrazodon_n	376	205	6.5	740	1	CT075_HUMAN	Q8wtu4_homo_sapien
304	212	6.8	276	2	Q4G1J9_EPTST	Q4g1j9_eptatretus	377	204.5	6.5	463	2	Q8C1V9_MOUSE	Q8c1v9_mus_musculus
305	212	6.8	445	2	Q80WD0_RAT	Q80wd0_rattus_norv	378	204	6.5	353	2	Q6QMY6_RAT	Q6qmy6_rattus_norv
306	212	6.8	918	2	Q7Q3F0_ANOGA	Q7q3f0_anopheles_g	379	204	6.5	1173	2	Q9V7J8_DROME	Q9v7j8_drosophila
307	211.5	6.7	192	2	Q6E4I9_PETMA	Q6E4i9_petromyzon	380	204	6.5	1306	2	Q6F4S1_XENLA	Q6pf4s1_xenopus_lae
308	211.5	6.7	270	2	Q6E4L7_PETMA	Q6E4l7_petromyzon	381	203.5	6.5	845	2	Q6A1I3_HUMAN	Q6a1i3_homo_sapien
309	211.5	6.7	518	2	Q5R712_PONPY	Q5r712_pongo_pygma	382	203.5	6.5	894	2	Q9VKG1_DROME	Q9vkgl1_drosophila
310	211	6.7	187	2	Q6E4I2_PETMA	Q6E4i2_petromyzon	383	203.5	6.5	1061	2	Q53ME4_ORYSA	Q53me4_oryza_sativ
311	211	6.7	581	1	LRTH3_HUMAN	Q86vh5_homo_sapien	384	203.5	6.5	1065	1	LRIG2_HUMAN	Q94998_homo_sapien
312	211	6.7	581	1	LRTH3_MACFA	Q9b9p6_macaca_fasc	385	203	6.5	269	2	Q6E4B6_PETMA	Q6E4b6_petromyzon
313	210.5	6.7	257	2	Q4G1M3_EPTBU	Q4g1m3_eptatretus	386	203	6.5	428	2	Q5NVQ6_PONPY	Q5nvq6_pongo_pygma
314	210.5	6.7	321	2	Q6E4L5_PETMA	Q6E4l5_petromyzon	387	203	6.5	602	2	Q4R3P6_MACFA	Q4r3p6_macaca_fasc
315	210.5	6.7	4303	1	PKDI_HUMAN	P98161_homo_sapien	388	203	6.5	703	2	Q4SLZ4_TETNG	Q4slz4_tetrazodon_n
316	210	6.7	358	1	CHAD_RAT	Q70210_rattus_norv	389	203	6.5	1514	2	Q6NN49_DROME	Q6nn49_drosophila
317	210	6.7	1028	2	Q86SR7_PIG	Q86sr7_sus_scrofa	390	203	6.5	1514	2	Q9NBK9_DROME	Q9nbk9_drosophila
318	209.5	6.7	214	2	Q6B4H0_PETMA	Q6E4h0_petromyzon	391	203	6.5	1514	2	Q9VUN0_DROME	Q9vun0_drosophila
319	209.5	6.7	533	2	Q5EST6_BOVIN	Q5est6_bos_taurus	392	202.5	6.5	259	2	Q4G1K1_EPTST	Q4g1k1_eptatretus
320	209	6.7	211	2	Q6E4I3_PETMA	Q6E4i3_petromyzon	393	202.5	6.5	259	2	Q4G1H5_EPTST	Q4g1h5_eptatretus
321	209	6.7	257	2	Q6E4J6_PETMA	Q6E4j6_petromyzon	394	202.5	6.5	274	2	Q6E4J2_PETMA	Q6E4j2_petromyzon
322	209	6.7	353	2	Q6UXK1_HUMAN	Q6uxk1_homo_sapien	395	202.5	6.5	829	2	Q4RIG0_TETNG	Q4rig0_tetrazodon_n
323	209	6.7	358	1	CHAD_MOUSE	Q55226_mus_musculus	396	202	6.4	271	2	Q4KPI1_LAMAP	Q4kpi1_lampetra_ap

397	6.4	202	1117	2	Q5VQM7_ORYSA	Q5vqm7	oryza sativ	470	194	6.2	692	2	Q4RV46_TETNG	Q4rv46	tetraodon n
398	201.5	6.4	187	2	Q6E4D7_PETMA	Q6e4d7	petromyzon	471	194	6.2	836	2	Q9V9V6_DROME	Q9v9v6	drosophila
399	201.5	6.4	275	2	Q4GLJ5_EPTST	Q4glj5	epitretus	472	193.5	6.2	186	2	Q6E4H8_PETMA	Q6e4h8	petromyzon
400	201.5	6.4	372	2	Q8CBR6_MOUSE	Q8cbr6	mus musculus	473	193.5	6.2	270	2	Q4KP03_LAMAP	Q4kp03	lampetra ap
401	201.5	6.4	457	2	Q960D1_DROME	Q960d1	drosophila	474	193.5	6.2	273	2	Q4GLM1_EPTBU	Q4glm1	epitretus
402	201.5	6.4	524	2	Q4RG59_TETNG	Q4rg59	tetraodon n	475	193.5	6.2	377	1	PRELP_RAT	Q4rgp5	rattus norv
403	201.5	6.4	551	2	Q4RF95_TETNG	Q4rf95	tetraodon n	476	193.5	6.2	378	2	Q8CA29_MOUSE	Q8ca29	mus musculus
404	201.5	6.4	606	2	Q9BZ20_HUMAN	Q9bz20	homo sapien	477	193.5	6.2	421	2	Q9NT99_HUMAN	Q9nt99	homo sapien
405	201.5	6.4	892	2	P91644_DROME	P91644	drosophila	478	193.5	6.2	433	2	Q61DGT_DROME	Q61dgt	drosophila
406	201.5	6.4	1527	2	Q9VZZA_DROME	Q9vzza	drosophila	479	193.5	6.2	545	1	LG12_HUMAN	Q8n0v4	homo sapien
407	201	6.4	213	2	Q6E4H6_PETMA	Q6e4h6	petromyzon	480	193.5	6.2	574	2	Q60W68_CAEBR	Q60w68	caenorhabdi
408	201	6.4	218	2	Q6E4K9_PETMA	Q6e4k9	petromyzon	481	193.5	6.2	721	1	Y20Z24_MYCBO	Q10690	mycobacteri
409	201	6.4	336	2	Q4S8M5_TETNG	Q4s8m5	tetraodon n	482	193.5	6.2	721	2	Q7TZ24_MYCBO	Q7tz24	mycobacteri
410	201	6.4	354	2	Q4W655_MOUSE	Q4w655	mus musculus	483	193.5	6.2	893	2	Q96C25_HUMAN	Q96c25	homo sapien
411	201	6.4	430	2	Q5BRT20_HUMAN	Q5btr20	homo sapien	484	193.5	6.2	910	2	Q9HB75_HUMAN	Q9hb75	homo sapien
412	201	6.4	581	2	Q9BTR7_HUMAN	Q9btr7	homo sapien	485	193.5	6.2	977	1	SLIK3_HUMAN	Q94933	homo sapien
413	201	6.4	602	2	Q9H9A6_HUMAN	Q9h9a6	homo sapien	486	193	6.2	252	2	Q4GL12_EPTST	Q4gl12	epitretus
414	201	6.4	712	2	Q5BL20_BRARE	Q5bl20	brachydanio	487	193	6.2	497	2	Q4S2U8_TETNG	Q4szu8	tetraodon n
415	200.5	6.4	845	1	SLIK2_HUMAN	Q9h156	homo sapien	488	193	6.2	540	2	Q9NK84_DROME	Q9nk84	drosophila
416	200	6.4	460	2	Q4RK03_TETNG	Q4rk03	tetraodon n	489	193	6.2	550	2	Q9VJN8_DROME	Q9vjn8	drosophila
417	200	6.4	616	2	Q58A95_CAEEL	Q58a95	caenorhabdi	490	192.5	6.1	187	2	Q6E4D5_PETMA	Q6e4d5	petromyzon
418	200	6.4	653	2	Q02329_CAEEL	Q02329	caenorhabdi	491	192.5	6.1	214	2	Q6E4G0_PETMA	Q6e4g0	petromyzon
419	199.5	6.4	227	2	Q4SP28_TETNG	Q4sp28	tetraodon n	492	192.5	6.1	259	2	Q4GLH7_EPTST	Q4glh7	epitretus
420	199.5	6.4	261	2	Q4GL14_EPTBU	Q4gl14	epitretus	493	192.5	6.1	270	2	Q6E4K0_PETMA	Q6e4k0	petromyzon
421	199.5	6.4	622	2	Q66HV9_BRARE	Q66hv9	brachydanio	494	192.5	6.1	428	2	Q6GU68_MOUSE	Q6gu68	mus musculus
422	199	6.3	846	1	SLIK2_MOUSE	Q810c0	mus musculus	495	192.5	6.1	542	2	Q50D27_MOUSE	Q50d27	mus musculus
423	199	6.3	862	2	Q4SST3_TETNG	Q4sst3	tetraodon n	496	192.5	6.1	575	2	Q2J580_CABEL	Q2j580	caenorhabdi
424	199	6.3	1328	2	Q21043_CAEEL	Q21043	caenorhabdi	497	192.5	6.1	1093	2	Q6HA06_CRAGI	Q6ha06	crassorhabdi
425	198.5	6.3	259	2	Q4GLJ4_EPTST	Q4glj4	epitretus	498	192	6.1	265	2	Q6E4K2_PETMA	Q6e4k2	petromyzon
426	198.5	6.3	320	2	Q6YN44_HUMAN	Q6yn44	homo sapien	499	192	6.1	273	2	Q6E4C5_PETMA	Q6e4c5	petromyzon
427	198.5	6.3	617	1	LRC21_RAT	Q9jmh2	rattus norv	500	192	6.1	548	1	LG13_MOUSE	Q8k406	mus musculus
428	198.5	6.3	741	2	Q4SWG9_TETNG	Q4swg9	tetraodon n	501	192	6.1	627	2	Q6UN14_LEICH	Q6un14	leishmania
429	198.5	6.3	873	2	Q7XR24_ORYSA	Q7xr24	oryza sativ	502	191.5	6.1	187	2	Q6E417_PETMA	Q6e417	petromyzon
430	198.5	6.3	1331	1	GP124_HUMAN	Q96pe1	homo sapien	503	191.5	6.1	204	2	Q6E4J8_PETMA	Q6e4j8	petromyzon
431	198	6.3	363	2	Q7SYE5_BRARE	Q7sy5e5	brachydanio	504	191.5	6.1	915	2	Q9ERV7_MOUSE	Q9erv7	mus musculus
432	198	6.3	602	2	Q5RFE9_PONPY	Q5rfe9	pongo pygma	505	191.5	6.1	980	1	SLIK3_MOUSE	Q810b9	mus musculus
433	197.5	6.3	280	2	Q6E4K3_PETMA	Q6e4k3	petromyzon	506	191.5	6.1	980	2	Q6NZM5_MOUSE	Q6nzm5	mus musculus
434	197.5	6.3	300	2	Q6E4K8_PETMA	Q6e4k8	petromyzon	507	191	6.1	271	2	Q4KP00_LAMAP	Q4kp00	lampetra ap
435	197.5	6.3	441	2	Q4VBZ3_HUMAN	Q4vbz3	homo sapien	508	191	6.1	440	2	Q5RC08_PONPY	Q5rcq8	pongo pygma
436	197.5	6.3	537	2	Q9VE49_DROME	Q9ve49	drosophila	509	191	6.1	610	2	Q4T1M0_TETNG	Q4tlm0	tetraodon n
437	197.5	6.3	548	1	LG13_HUMAN	Q8n145	homo sapien	510	190.5	6.1	251	2	Q4GL17_EPTST	Q4gl17	epitretus
438	197.5	6.3	548	1	Q4R4H3_MACFA	Q4r4h3	macaca fasc	511	190.5	6.1	894	2	Q5H721_FUGRU	Q5h721	fugu rubrip
439	197.5	6.3	818	2	Q4SIX2_TETNG	Q4si2	tetraodon n	512	190.5	6.1	1238	2	Q6NR19_DROME	Q6nr19	drosophila
440	197.5	6.3	835	2	Q4SFB0_TETNG	Q4sfb0	tetraodon n	513	190.5	6.1	1535	2	Q9VPF0_DROME	Q9vpf0	drosophila
441	197.5	6.3	1321	1	GP125_HUMAN	Q81wk6	homo sapien	514	190	6.1	191	2	Q6E4H3_PETMA	Q6e4h3	petromyzon
442	197	6.3	345	2	Q9HBL6_HUMAN	Q9hbl6	homo sapien	515	190	6.1	639	2	Q4RE68_TETNG	Q4re68	tetraodon n
443	197	6.3	694	2	Q6YXX5_ORYSA	Q6yxx5	oryza sativ	516	190	6.1	654	2	Q6Z8N6_CAEBR	Q6z8n6	caenorhabdi
444	197	6.3	1093	2	Q5XWD3_HUMAN	Q5xwd3	homo sapien	517	190	6.1	733	1	CT075_MOUSE	P59383	mus musculus
445	196.5	6.3	259	2	Q4GLJ3_EPTST	Q4glj3	epitretus	518	190	6.1	1119	1	LRIG3_HUMAN	Q6uxm1	homo sapien
446	196.5	6.3	261	2	Q4GLJ7_EPTST	Q4glj7	epitretus	519	190	6.1	1346	2	Q9V477_DROME	Q9v477	drosophila
447	196	6.3	263	2	Q6E4D0_PETMA	Q6e4d0	petromyzon	520	190	6.1	2800	2	Q6XHB1_DICDI	Q6xnb1	dictyosteli
448	196	6.3	3638	2	Q15142_HUMAN	Q15142	homo sapien	521	189.5	6.0	252	2	Q4GLJ7_EPTST	Q4glj7	epitretus
449	195.5	6.2	370	2	Q58DI7_BOVIN	Q58di7	bos taurus	522	189.5	6.0	370	2	Q4RSX9_TETNG	Q4rsx9	tetraodon n
450	195.5	6.2	378	1	PRELP_MOUSE	Q91k53	mus musculus	523	189	6.0	369	1	PGS1_MOUSE	P28653	mus musculus
451	195.5	6.2	378	2	Q543S0_MOUSE	Q543s0	mus musculus	524	189	6.0	369	1	PGS1_RAT	P47853	rattus norv
452	195.5	6.2	917	2	Q86FM1_DROME	Q86fm1	drosophila	525	189	6.0	627	2	Q4T5R5_TETNG	Q4t5r5	tetraodon n
453	195.5	6.2	931	2	Q9VM16_DROME	Q9vpm1	drosophila	526	189	6.0	760	2	Q4QG18_LEIMA	Q4qg18	leishmania
454	195	6.2	440	2	Q4R5H2_MACFA	Q4r5h2	macaca fasc	527	189	6.0	839	2	Q9SN46_ARATH	Q9sn46	arabidopsis
455	195	6.2	614	2	Q6NUK3_HUMAN	Q6nuk3	homo sapien	528	189	6.0	1392	2	Q9VAD1_DROME	Q9vad1	drosophila
456	195	6.2	620	2	Q6UXM3_HUMAN	Q6uxm3	homo sapien	529	189	6.0	4311	2	Q7YOK5_CANFA	Q7yok5	canis fami
457	195	6.2	837	1	SLIK4_HUMAN	Q81w52	homo sapien	530	188.5	6.0	369	2	Q6GM15_BRARE	Q6gm15	brachydanio
458	195	6.2	837	2	Q5XKG3_HUMAN	Q51xg3	homo sapien	531	188.5	6.0	370	2	Q504E0_BRARE	Q504e0	brachydanio
459	194.5	6.2	369	2	Q65Z91_CHICK	Q65z91	gallus gall	532	188.5	6.0	410	2	Q9DDZ7_PETMA	Q9ddz7	petromyzon
460	194.5	6.2	693	2	Q7Z3D0_HUMAN	Q7z3d0	homo sapien	533	188.5	6.0	433	2	Q5SYH5_MOUSE	Q5syh5	mus musculus
461	194.5	6.2	699	1	ECM2_HUMAN	Q94769	homo sapien	534	188.5	6.0	440	1	OMGP_MOUSE	Q63912	mus musculus
462	194.5	6.2	699	2	Q5T9F2_HUMAN	Q5t9f2	homo sapien	535	188.5	6.0	538	2	Q5Z8W0_ORYSA	Q5z8w0	oryza sativ
463	194.5	6.2	737	2	Q965M3_CAEEL	Q965m3	caenorhabdi	536	188.5	6.0	655	2	Q4SBU9_TETNG	Q4sbu9	tetraodon n
464	194.5	6.2	881	2	Q965M2_CAEEL	Q965m2	caenorhabdi	537	188	6.0	368	2	Q4SBU9_TETNG	Q4sbu9	tetraodon n
465	194.5	6.2	1630	1	LAP4_HUMAN	Q14160	homo sapien	538	188	6.0	369	1	PGS1_CANFA	Q02678	canis fami
466	194	6.2	258	2	Q4GLI0_EPTST	Q4glj0	epitretus	539	188	6.0	369	2	Q7TWM3_MOUSE	Q7tmw3	mus musculus
467	194	6.2	258	2	Q4GLI0_EPTST	Q4glj0	epitretus	540	188	6.0	522	1	LRTM1_MOUSE	Q8k377	mus musculus
468	194	6.2	263	2	Q6B4C0_PETMA	Q6e4c0	petromyzon	541	188	6.0	626	2	Q4SE92_TETNG	Q4se92	tetraodon n
469	194	6.2	611	2	Q4RHK3_TETNG	Q4rhk3	tetraodon n	542	188	6.0	818	2	Q5ZIH8_CHICK	Q5zih8	gallus gall

543	187.5	6.0	259	2	Q4GL10_EPTBU	Q4g110 eptatretus	616	183	5.8	568	2	Q6P3Y9_MOUSE	Q6p3y9 mus musculus
544	187.5	6.0	310	2	Q9DDZ8_PETMA	Q9ddz8 petromyzon	617	183	5.8	662	1	LRC312_HUMAN	LRC312 homo sapien
545	187.5	6.0	350	2	Q5M7S9_XENTR	Q5m7s9 xenopus tro	618	183	5.8	664	2	Q7ZT81_ONCMY	Q7zt81 oncorhynchus
546	187.5	6.0	352	2	Q4W6V7_CHICK	Q4w6v7 gallus gall	619	183	5.8	672	2	O5ZJ34_CHICK	O5zj34 gallus gall
547	187.5	6.0	363	2	Q9H5G9_HUMAN	Q9h5g9 homo sapien	620	182.5	5.8	872	2	Q6E4G3_PETMA	Q6e4g3 petromyzon
548	187.5	6.0	435	2	Q9VGH2_DROME	Q9vgh2 drosophila	621	182.5	5.8	187	2	Q6E4G7_PETMA	Q6e4g7 petromyzon
549	187.5	6.0	601	2	Q7SXW3_BRARE	Q7sxw3 brachydanio	622	182.5	5.8	257	2	Q4GL18_EPTBU	Q4gl18 eptatretus
550	187.5	6.0	861	2	Q4ZJ82_CHICK	Q4zj82 gallus gall	623	182.5	5.8	379	1	ASPN_HUMAN	Q9bxi1 homo sapien
551	187	6.0	260	2	Q4GLK7_EPTST	Q4glk7 eptatretus	624	182.5	5.8	380	2	O5BTF3_HUMAN	Q5btf3 homo sapien
552	187	6.0	262	2	Q4GLK0_EPTST	Q4glk0 eptatretus	625	182.5	5.8	384	2	O6P528_HUMAN	Q6p528 homo sapien
553	187	6.0	592	2	Q61PG4_CABER	Q61pg4 caenorhabdi	626	182.5	5.8	810	2	O8T3J2_DROME	O8t3j2 drosophila
554	187	6.0	615	2	Q9VZ84_DROME	Q9vz84 drosophila	627	182.5	5.8	811	2	Q9VK54_DROME	Q9vk54 drosophila
555	187	6.0	735	2	Q6E1I4_MOUSE	Q6e1i4 mus musculus	628	182.5	5.8	828	1	TLR4_PONPY	Q8sep9 pongo pygma
556	187	6.0	818	2	Q5WAJ2_CHICK	Q5waj2 gallus gall	629	182.5	5.8	837	1	TLR4_GORGO	Q8sep8 gorilla gor
557	187	6.0	1741	2	Q5LJU2_DROME	Q5lju2 drosophila	630	182.5	5.8	880	2	P91643_DROME	P91643 drosophila
558	186.5	5.9	368	1	PGS1_XENLA	Q9ib75 xenopus lae	631	182.5	5.8	958	1	SLIK5_HUMAN	Q94991 homo sapien
559	186.5	5.9	521	2	Q72U34_LEPIC	Q72u34 leptospira	632	182.5	5.8	958	2	O5VT81_HUMAN	O5vt81 homo sapien
560	186.5	5.9	639	2	Q5VZ17_HUMAN	Q5vz17 homo sapien	633	182.5	5.8	958	2	Q4QOH1_HUMAN	Q4qoh1 homo sapien
561	186.5	5.9	799	2	Q5VZ18_HUMAN	Q5vz18 homo sapien	634	182	5.8	205	2	Q4R9X7_TETNG	Q4r9x7 tetraodon n
562	186.5	5.9	839	1	TLR4_HUMAN	Q00206 homo sapien	635	182	5.8	252	2	Q4GL18_EPTST	Q4gl18 eptatretus
563	186.5	5.9	839	1	TLR4_PANPA	Q9tt10 pan paniscu	636	182	5.8	271	2	Q6E4C4_PETMA	Q6e4c4 petromyzon
564	186.5	5.9	839	2	Q5VZ19_HUMAN	Q5vz19 homo sapien	637	182	5.8	297	2	Q4RU73_TETNG	Q4ru73 tetraodon n
565	186	5.9	273	2	Q6E4B4_PETMA	Q6e4b4 petromyzon	638	182	5.8	369	1	PGS1_SHEEP	O46390 ovis aries
566	186	5.9	368	2	O5RAY4_PONPY	Q5ray4 pongo pygma	639	182	5.8	369	2	Q5BIM3_BOVIN	Q5bim3 bos taurus
567	186	5.9	440	1	OMGD_HUMAN	P23315 homo sapien	640	182	5.8	373	2	Q803T1_BRARE	Q803t1 brachydanio
568	186	5.9	440	2	Q53HB8_HUMAN	Q53hb8 homo sapien	641	182	5.8	373	2	Q5RI45_BRARE	Q5ri45 brachydanio
569	186	5.9	552	2	Q9VT44_DROME	Q9vt44 drosophila	642	182	5.8	428	2	O8P3F8_LEPIN	O8p3f8 leptospira
570	186	5.9	623	1	LRC21_HUMAN	Q9p2v4 homo sapien	643	182	5.8	532	2	O96671_DROME	O96671 drosophila
571	186	5.9	1029	2	O512M5_BOVIN	O5i2m5 bos taurus	644	182	5.8	678	2	Q7Q550_ANOGA	Q7q550 anopheles g
572	185.5	5.9	369	2	Q4T3M1_TETNG	Q4t3m1 tetraodon n	645	182	5.8	1022	2	Q8HXV0_BOVIN	Q8hxxv0 bos taurus
573	185.5	5.9	466	2	Q6W1W3_XENLA	Q6w1w3 xenopus lae	646	182	5.8	1029	2	Q866B2_BOVIN	Q866b2 bos taurus
574	185.5	5.9	953	2	Q6MF87_PARUW	Q6mf87 parachlamyd	647	181.5	5.8	180	2	Q8BPJ0_MOUSE	Q8bpj0 mus musculus
575	185	5.9	254	2	Q4S4N7_TETNG	Q4s4n7 tetraodon n	648	181.5	5.8	251	2	Q4GLK2_EPTST	Q4glk2 eptatretus
576	185	5.9	389	2	Q6BP5_BRARE	Q6bp5 brachydanio	649	181.5	5.8	259	2	Q4GLJ8_EPTST	Q4glj8 eptatretus
577	185	5.9	512	2	Q6PEZ8_HUMAN	Q6pez8 homo sapien	650	181.5	5.8	357	1	PGS2_CHICK	P28675 gallus gall
578	185	5.9	603	2	Q5LJN0_CHICK	Q5ljn0 gallus gall	651	181.5	5.8	599	2	Q7T3H6_BRARE	Q7t3h6 brachydanio
579	184.5	5.9	257	2	Q4GL15_EPTBU	Q4gl15 eptatretus	652	181.5	5.8	699	2	Q61PG3_CABER	Q61pg3 caenorhabdi
580	184.5	5.9	270	2	Q4FP09_LAMAP	Q4fp09 lampetra ap	653	181.5	5.8	2160	2	O13328_MAGGR	O13328 magnaporthe
581	184.5	5.9	724	2	Q5XWB9_HORSE	Q5xwb9 equus cabal	654	181.5	5.8	2160	2	O13488_MAGGR	O13488 magnaporthe
582	184.5	5.9	799	2	Q9V964_DROME	Q9v964 drosophila	655	181.5	5.8	2160	2	O51J05_MAGGR	O51j05 magnaporthe
583	184.5	5.9	839	2	Q69ZV6_MOUSE	Q69zv6 mus musculus	656	181	5.8	372	1	PGS1_HORSE	Q46403 equus cabal
584	184.5	5.9	841	2	Q5F4K7_PIG	Q5f4k7 sus scrofa	657	181	5.8	569	2	Q7QIP3_ANOGA	Q7qip3 anopheles g
585	184.5	5.9	843	1	TLR4_HORSE	Q9m7w3 equus cabal	658	181	5.8	1013	2	Q8LQ10_ORYSA	Q8lq10 oryza sativ
586	184.5	5.9	957	1	SLIK5_MOUSE	Q810b7 mus musculus	659	181	5.8	1333	2	Q7Q168_ANOGA	Q7q168 anopheles g
587	184.5	5.9	1007	2	Q65XS3_ORYSA	Q65xs3 oryza sativ	660	180.5	5.8	371	2	O6GLQ6_XENLA	O6glq6 xenopus lae
588	184.5	5.9	1046	2	Q5G097_CHICK	Q5g097 gallus gall	661	180.5	5.8	385	2	Q8BMW6_MOUSE	Q8bmw6 mus musculus
589	184.5	5.9	1214	2	Q6JUN6_ORYSA	Q6jun6 oryza sativ	662	180.5	5.8	441	2	Q81170_DROVI	Q81170 drosophila
590	184	5.9	187	2	Q6E4M5_PETMA	Q6e4m5 petromyzon	663	180.5	5.8	522	1	AMGO2_PONPY	Q8bmw6 mus musculus
591	184	5.9	253	2	Q6E4K5_PETMA	Q6e4k5 petromyzon	664	180.5	5.8	584	2	Q6PGX3_BRARE	Q6pgx3 pongo pygma
592	184	5.9	263	2	Q4E4K7_PETMA	Q4e4k7 petromyzon	665	180.5	5.8	821	2	Q9VPY3_HUMAN	Q9vpy3 homo sapien
593	184	5.9	274	2	Q4GLM0_EPTBU	Q4glm0 eptatretus	666	180.5	5.8	1443	2	Q9VJQ0_DROME	Q9vjq0 drosophila
594	184	5.9	291	2	Q4RF21_TETNG	Q4rf21 tetraodon n	667	180.5	5.8	1460	2	Q5H261_XENTR	Q5h261 xenopus tro
595	184	5.9	368	1	PGS1_HUMAN	P21810 homo sapien	668	180	5.7	250	2	Q4G1M2_EPTBU	Q4g1m2 eptatretus
596	184	5.9	368	2	Q53F14_HUMAN	Q53f14 homo sapien	669	180	5.7	369	1	PGS1_BOVIN	Q21809 bos taurus
597	184	5.9	473	2	Q7QF76_ANOGA	Q7qf76 anopheles g	670	180	5.7	522	1	LRTM1_PONPY	Q5x6b1 pongo pygma
598	184	5.9	543	2	Q4RGC6_TETNG	Q4rgc6 petromyzon	671	180	5.7	817	2	Q86P15_DROME	Q86p15 drosophila
599	184	5.9	552	2	Q6K6X6_ORYSA	Q6k6x6 oryza sativ	672	180	5.7	817	2	Q9VS84_DROME	Q9ve84 drosophila
600	184	5.9	565	2	Q7PJD0_ANOGA	Q7pjd0 anopheles g	673	180	5.7	843	2	Q7ZTGS_CHICK	Q7ztgs gallus gall
601	184	5.9	837	1	SLIK4_MOUSE	Q810b8 mus musculus	674	180	5.7	869	2	Q4S0C1_TETNG	Q4s0c1 tetraodon n
602	183.5	5.9	187	2	Q6E4F6_PETMA	Q6e4f6 petromyzon	675	179.5	5.7	872	2	Q6E4D6_PETMA	Q6e4d6 petromyzon
603	183.5	5.9	287	2	Q9W2B9_DROME	Q9w2b9 drosophila	676	179.5	5.7	585	2	Q61GX3_CABER	Q61gx3 caenorhabdi
604	183.5	5.9	292	2	Q6NYI6_BRARE	Q6nyi6 brachydanio	677	179.5	5.7	820	2	Q5R3F8_HUMAN	Q5r3f8 homo sapien
605	183.5	5.9	601	2	Q6TLH1_BRARE	Q6tlh1 brachydanio	678	179.5	5.7	1117	1	L3IG3_MOUSE	Q6l3c6 mus musculus
606	183.5	5.9	652	2	Q7O696_ANOGA	Q7o696 anopheles g	679	179.5	5.7	4283	2	Q9ERV0_RAT	Q9erv0 rattus norv
607	183.5	5.9	727	2	Q6A0E8_MOUSE	Q6a0e8 mus musculus	680	179	5.7	273	2	Q6E4B6_PETMA	Q6e4b6 petromyzon
608	183.5	5.9	795	1	TLR1_MOUSE	Q9epq1 mus musculus	681	179	5.7	314	2	Q5M8M9_MOUSE	Q5m8m9 mus musculus
609	183.5	5.9	824	2	Q5GGX1_PIG	Q5ggx1 sus scrofa	682	179	5.7	534	2	Q9VT89_DROME	Q9vt89 drosophila
610	183.5	5.9	841	1	TLR4_PIG	Q69y56 sus scrofa	683	179	5.7	700	2	O9P244_HUMAN	O9p244 homo sapien
611	183.5	5.9	1059	2	O5ZJD0_CHICK	O5zjd0 gallus gall	684	179	5.7	742	2	Q9BJD4_STRPU	Q9bjd4 strongyloce
612	183.5	5.9	1495	2	Q5VXC2_HUMAN	Q5vxc2 homo sapien	685	179	5.7	905	1	TLR3_MOUSE	Q99mb1 mus musculus
613	183.5	5.9	1537	1	LRRC7_HUMAN	Q96nw7 homo sapien	686	179	5.7	969	2	Q4LBC9_ONCMY	Q4lbc9 oncorhynchus
614	183.5	5.9	1537	2	Q5VXC3_HUMAN	Q5vxc3 homo sapien	687	179	5.7	1029	2	Q512M4_SHEEP	Q512m4 ovis aries
615	183	5.8	540	2	Q9VU53_DROME	Q9vu53 drosophila	688	178.5	5.7	176	2	Q567L5_BRARE	Q567l5 brachydanio

689	178.5	5.7	190	2	Q6E4D8_PETMA	Q6E4d8 petromyzon	762	174.5	5.6	440	2	Q4J5V4_AZOVI	Q4J5v4 azotobacter
690	178.5	5.7	348	2	Q5R143_BRARE	Q5r143 brachydanio	763	174.5	5.6	512	2	Q3CQ76_MOUSE	Q3cq76 m mus muscu
691	178.5	5.7	356	1	PGS2_COTJA	Q9de68 coturnix co	764	174.5	5.6	567	2	Q4B110_TETNG	Q4b110 tetraodon n
692	178.5	5.7	443	1	Q67VV7_ORYSA	Q67vv7 oryza sativ	765	174.5	5.6	602	2	Q3CRC8_MOUSE	Q3crc8 mus musculus
693	178.5	5.7	493	1	AMGO1_HUMAN	Q86wk6 homo sapien	766	174.5	5.6	602	2	Q8BS83_MOUSE	Q8be83 mus musculus
694	178.5	5.7	587	1	Q4OGJ9_LETMA	Q4ggj9 leishmania	767	174.5	5.6	602	2	Q78WQ9_MOUSE	Q78wq9 mus musculus
695	178.5	5.7	1024	1	POPC_RALSO	Q97ba2 ralstonia s	768	174.5	5.6	605	2	Q6GPJ5_XENLA	Q6gpj5 xenopus lae
696	178.5	5.7	1063	2	Q5Z6G6_ORYSA	Q5z666 oryza sativ	769	174.5	5.6	795	1	TLR6_MOUSE	Q6epw9 mus musculus
697	178.5	5.7	1104	2	Q7XUH4_ORYSA	Q7xuh4 oryza sativ	770	174.5	5.6	1020	2	Q5ZED4_ORYSA	Q5zed4 oryza sativ
698	178.5	5.7	1310	1	GP125_MOUSE	Q7tt36 mus musculus	771	174.5	5.6	1060	2	Q6ZGM3_ORYSA	Q6zgm3 oryza sativ
699	178	5.7	187	2	Q6E4H4_PETMA	Q6e4h4 petromyzon	772	174	5.6	490	2	Q4RYL5_TETNG	Q4ryl5 tetraodon n
700	178	5.7	364	2	Q6GJ59_XENLA	Q6gj59 xenopus lae	773	174	5.6	535	2	Q8RX50_BRANI	Q8rx50 brassica ni
701	178	5.7	391	2	Q4RQ11_TETNG	Q4rq11 tetraodon n	774	174	5.6	544	2	Q7Q2W5_ANOGA	Q7q2w5 anopheles g
702	178	5.7	488	2	Q4RXQ2_TETNG	Q4rxq2 tetraodon n	775	174	5.6	651	2	Q4JQQ2_XENLA	Q4jqq2 xenopus lae
703	178	5.7	522	1	LRTM1_HUMAN	Q86ue6 homo sapien	776	174	5.6	859	1	TLR5_MOUSE	Q9jlf7 mus musculus
704	178	5.7	894	2	Q9BJD6_STRPU	Q9bjd6 strongyloce	777	174	5.6	951	1	LGR4_RAT	Q9z2h4 rattus norv
705	178	5.7	1049	1	TLR7_HUMAN	Q9nyk1 homo sapien	778	173.5	5.5	261	2	Q5M8T1_HUMAN	Q5m8t1 homo sapien
706	178	5.7	1052	2	Q9Y4C4_HUMAN	Q9y4c4 homo sapien	779	173.5	5.5	337	2	Q4RJX0_TETNG	Q4rxj0 tetraodon n
707	178	5.7	1257	2	Q7PNF8_ANOGA	Q7pnf8 anopheles g	780	173.5	5.5	353	2	Q640B1_XENTR	Q640b1 xenopus tro
708	177.5	5.7	275	2	Q4G1K5_EPTST	Q4g1k5 eptatretus	781	173.5	5.5	364	2	Q6GNX8_XENLA	Q6gnx8 xenopus lae
709	177.5	5.7	796	2	Q59HI9_PIG	Q59hi9 sus scrofa	782	173.5	5.5	421	1	OMD_HUMAN	Q999x8 homo sapien
710	177.5	5.7	796	2	Q4LDR7_PIG	Q4ldr7 sus scrofa	783	173.5	5.5	421	2	Q5TBF4_HUMAN	Q5tbf4 homo sapien
711	177.5	5.7	809	2	Q4RMO1_TETNG	Q4rmq1 tetraodon n	784	173.5	5.5	440	2	Q7TQ25_RAT	Q7tg25 rattus norv
712	177.5	5.7	1026	2	Q5SMW2_ORYSA	Q5smw2 oryza sativ	785	173.5	5.5	537	1	LG14_MOUSE	Q8k1s1 mus musculus
713	177.5	5.7	1050	1	TLR7_MOUSE	P59681 mus musculus	786	173.5	5.5	727	2	Q6GV21_BOVIN	Q6gv21 bos taurus
714	177.5	5.7	1050	2	Q548J0_MOUSE	Q548j0 mus musculus	787	173.5	5.5	806	2	Q7TPC5_MOUSE	Q7tpc5 mus musculus
715	177.5	5.7	1360	2	Q7KTA0_DROME	Q7kta0 drosophila	788	173.5	5.5	826	1	TLR4_PAPAN	Q7esp2 papio anubi
716	177.5	5.7	1530	2	Q6BD07_HUMAN	Q6bd07 homo sapien	789	173.5	5.5	884	2	Q5H720_FUGRU	Q5h720 fugu rubrip
717	177.5	5.7	2300	1	CYAA_NEUCR	P01631 neurospora	790	173	5.5	252	2	Q4G114_EPTST	Q4g114 eptatretus
718	177.5	5.7	2493	1	CYAA_USTMA	P49606 ustilago ma	791	173	5.5	269	2	Q6E4C2_PETMA	Q6e4c2 petromyzon
719	177.5	5.7	2493	2	Q4P3T1_USTMA	Q4p3t1 ustilago ma	792	173	5.5	360	1	PGS2_HORSE	Q46542 equus cabal
720	177	5.6	187	2	Q6E4H5_PETMA	Q6e4h5 petromyzon	793	173	5.5	470	2	Q9V354_DROME	Q9v354 drosophila
721	177	5.6	334	2	Q4S8U8_TETNG	Q4s8u8 tetraodon n	794	173	5.5	539	2	Q503F6_BRARE	Q503f6 brachydanio
722	177	5.6	343	1	LUM_COTJA	Q9de67 coturnix co	795	173	5.5	664	2	Q5UT54_SALSA	Q5ut54 salmo salar
723	177	5.6	347	2	Q58A48_BRARE	Q58a48 brachydanio	796	173	5.5	853	2	Q8CB40_MOUSE	Q8cb40 mus musculus
724	177	5.6	662	2	Q5RF01_PONPY	Q5rf01 pongo pygma	797	173	5.5	925	1	GLHR_ATEL	P35409 antrophleura
725	177	5.6	666	2	Q7Q2M6_ANOGA	Q7q2m6 anopheles g	798	173	5.5	1459	2	Q7Q0C5_ANOGA	Q7q0c5 anopheles g
726	177	5.6	670	2	Q5FW83_MOUSE	Q5fw85 mus musculus	799	173	5.5	1459	2	Q8WR54_ANOGA	Q8wre4 anopheles g
727	177	5.6	1370	2	Q58NA4_APIME	Q58na4 apis mellif	800	172.5	5.5	163	2	Q6E4E2_PETMA	Q6e4e2 petromyzon
728	176.5	5.6	187	2	Q6E4M0_PETMA	Q6e4m0 petromyzon	801	172.5	5.5	353	1	KERA_CHICK	Q42335 gallus gall
729	176.5	5.6	520	2	Q5VR46_ORYSA	Q5vr46 oryza sativ	802	172.5	5.5	353	1	KERA_COTJA	Q9de66 coturnix co
730	176.5	5.6	522	1	AMGO2_HUMAN	Q86sj2 homo sapien	803	172.5	5.5	359	1	PGS2_HUMAN	P07585 homo sapien
731	176.5	5.6	522	2	Q4VBP6_HUMAN	Q4vbp6 homo sapien	804	172.5	5.5	359	1	PGS2_PANTR	Q5rlv9 pan troglod
732	176.5	5.6	628	2	Q7PVZ6_ANOGA	Q7pvz6 anopheles g	805	172.5	5.5	359	2	Q6FH10_HUMAN	Q6fh10 homo sapien
733	176.5	5.6	856	2	Q59HI7_PIG	Q59hi7 sus scrofa	806	172.5	5.5	378	2	Q5R294_DROSI	Q5r294 drosophila
734	176.5	5.6	901	2	Q4SBD4_TETNG	Q4sbd4 tetraodon n	807	172.5	5.5	739	2	Q6ONV9_CABBR	Q6onv9 caenorhabdi
735	176.5	5.6	1495	1	LRRCT_RAT	P70587 rattus norv	808	172.5	5.5	823	2	Q8CCW8_MOUSE	Q8ccw8 mus musculus
736	176.5	5.6	1756	2	Q6AWK6_DROME	Q6awk6 drosophila	809	172.5	5.5	823	2	Q68FM6_MOUSE	Q68fm6 mus musculus
737	176	5.6	249	2	Q4SUM4_TETNG	Q4sum4 tetraodon n	810	172.5	5.5	1711	2	Q59DT7_DROME	Q59dt7 drosophila
738	176	5.6	503	2	Q8LJ87_ORYSA	Q8lj87 oryza sativ	811	172.5	5.5	1850	2	Q59DT8_DROME	Q59dt8 drosophila
739	176	5.6	623	2	Q95S21_DROME	Q95s21 drosophila	812	172.5	5.5	1851	1	LAP4_DROME	Q7kry7 drosophila
740	176	5.6	862	2	Q5GR02_CHICK	Q5gr02 gallus gall	813	172.5	5.5	4256	2	Q8MJF3_CANFA	Q8mjf3 canis famli
741	176	5.6	904	2	Q5TJ58_BOVIN	Q5tj58 bos taurus	814	172	5.5	339	2	Q4SU68_TETNG	Q4su68 tetraodon n
742	176	5.6	905	2	Q5TJ58_BOVIN	Q5tj58 bos taurus	815	172	5.5	347	2	Q7ZUT1_BRARE	Q7zut1 brachydanio
743	176	5.6	906	2	Q45RZ0_TETNG	Q4srz0 tetraodon n	816	172	5.5	411	2	Q4S9P3_TETNG	Q4s9p3 tetraodon n
744	176	5.6	1032	2	Q5T2M8_CANFA	Q5t2m8 canis famli	817	172	5.5	577	2	Q8N3K5_HUMAN	Q8n3k5 homo sapien
745	176	5.6	1257	2	Q9VK28_DROME	Q9vk28 drosophila	818	172	5.5	1134	2	Q65510_ARATH	Q65510 arabidopsis
746	176	5.6	1412	1	LAP2_HUMAN	Q96rt1 homo sapien	819	172	5.5	1693	2	Q4INH4_GIBRE	Q4inh4 gibberella
747	175.5	5.6	272	2	Q4KP14_9PETR	Q4kp14 ichtyomyzo	820	171.5	5.5	378	2	Q9V900_DROME	Q9v900 drosophila
748	175.5	5.6	384	2	Q4T0V4_TETNG	Q4t0v4 tetraodon n	821	171.5	5.5	605	2	Q5M8G4_XENTR	Q5m8g4 xenopus tro
749	175.5	5.6	440	2	Q7TNM3_RAT	Q7tnm3 rattus norv	822	171.5	5.5	683	1	LSC4_HUMAN	Q75427 homo sapien
750	175.5	5.6	492	1	AMGO1_MOUSE	Q80zd8 mus musculus	823	171.5	5.5	858	1	TLR5_HUMAN	Q60602 homo sapien
751	175.5	5.6	1017	2	Q5H718_FUGRU	Q5h718 fugu rubrip	824	171.5	5.5	858	2	Q5U308_RAT	Q5u308 rattus norv
752	175.5	5.6	1490	1	LRRCT_MOUSE	Q80te7 mus musculus	825	171.5	5.5	859	1	LRRCS_MOUSE	Q8bgr2 mus musculus
753	175.5	5.6	1731	2	Q4S0D3_TETNG	Q4s0d3 tetraodon n	826	171.5	5.5	1589	2	Q9UUQ9_METAN	Q9uud9 sus scrofa
754	175	5.6	252	2	Q4GLJ2_EPTST	Q4glj2 eptatretus	827	171	5.5	360	1	PGS2_PIG	Q9uxd9 sus scrofa
755	175	5.6	343	1	LUM_CHICK	P51890 gallus gall	828	171	5.5	360	2	Q6DV11_GECJA	Q6dv11 gecko japon
756	175	5.6	429	2	Q8BJ09_MOUSE	Q8bj09 mus musculus	829	171	5.5	552	2	Q86V06_HUMAN	Q86v06 homo sapien
757	175	5.6	510	2	Q9BGY6_MACFA	Q9bgy6 macaca fasc	830	171	5.5	643	2	Q502J4_BRARE	Q502j4 brachydanio
758	175	5.6	941	2	Q5H722_FUGRU	Q5h722 fugu rubrip	831	171	5.5	833	1	TLR4_FELCA	Q502j4 felis silve
759	175	5.6	973	2	Q6KCC7_ONCMY	Q6kcc7 oncorhynch	832	171	5.5	1317	2	Q5TUS9_ANOGA	P58727 anopheles g
760	175	5.6	1137	2	Q7QHH1_ANOGA	Q7qhh1 anopheles g	833	170.5	5.4	246	2	Q6E4J1_PETMA	Q6e4j1 petromyzon
761	174.5	5.6	190	2	Q6E4E5_PETMA	Q6e4e5 petromyzon	834	170.5	5.4	359	2	Q4R5D2_MACFA	Q4r5d2 macaca fasc

981	164	5.2	696	2	Q5RAC4_PONPY	Q5rac4	pongo pygma	1054	161	5.1	1019	2	Q4RW99_TETNG	Q4rw99	tetraodon n
982	164	5.2	760	2	Q63Z70_MOUSE	Q63z70	mus musculus	1055	160.5	5.1	487	2	Q7QKY2_ANOGA	Q7ky2	anopheles g
983	164	5.2	805	2	Q7QFF0_ANOGA	Q7qff0	anopheles g	1056	160.5	5.1	519	1	AMGO2_MOUSE	Q80zd9	mus musculus
984	164	5.2	828	1	LGR6_HUMAN	Q9hbx8	homo sapien	1057	160.5	5.1	519	2	Q4VB66_MOUSE	Q4vbe6	mus musculus
985	164	5.2	833	2	Q7Q8I8_ANOGA	Q7q8i8	anopheles g	1058	160.5	5.1	1446	2	Q5EWY7_CTEID	Q5ewy7	ctenopharyn
986	164	5.2	839	2	Q8MIQ2_RABIT	Q8miq2	oryctolagus	1059	160.5	5.1	666	2	Q9V8Z0_DROME	Q9v8z0	drosophila
987	164	5.2	870	2	Q6PCD4_HUMAN	Q6pcd4	homo sapien	1060	160.5	5.1	2910	2	O55225_MOUSE	O55225	mus musculus
988	164	5.2	904	1	TLR3_HUMAN	O15455	homo sapien	1061	160.5	5.1	3889	2	Q6SSB8_CHLRE	Q6sse8	chlamydomon
989	164	5.2	904	2	Q504W0_HUMAN	Q504w0	homo sapien	1062	160	5.1	258	2	Q4GLJ6_EPTST	Q4glj6	eptatretus
990	164	5.2	904	2	Q4VAL2_HUMAN	Q4val2	homo sapien	1063	160	5.1	518	2	Q4R5R9_MACFA	Q4r5r9	macaca fasc
991	164	5.2	1032	2	Q865B9_CANFA	Q865b9	canis famil	1064	160	5.1	744	2	O65375_ARATH	O65375	arabidopsis
992	164	5.2	1395	2	Q7SC01_NEUCR	Q7sc01	neurospora	1065	160	5.1	950	2	O5H723_FUGRU	O5h723	fugu rubrip
993	164	5.2	1913	2	O5SVA2_HUMAN	O5ava2	homo sapien	1066	160	5.1	1050	2	Q9BN18_DROME	Q9bn18	drosophila
994	164	5.2	2045	1	AGRN_HUMAN	O00468	homo sapien	1067	160	5.1	1080	2	Q69P46_ORYSA	Q69p46	oryza sativ
995	164	5.2	2045	2	Q60FEI_HUMAN	Q60fe1	homo sapien	1068	160	5.1	1096	2	Q8W556_ARATH	Q8w556	arabidopsis
996	163.5	5.2	163	2	Q6E4I0_PETMA	Q6e4i0	petromyzon	1069	160	5.1	1402	1	LAP2_MOUSE	Q80th2	mus musculus
997	163.5	5.2	166	2	Q6E4H7_PETMA	Q6e4h7	petromyzon	1070	160	5.1	1496	2	Q92626_HUMAN	Q92626	homo sapien
998	163.5	5.2	180	2	Q6E4H7_PETMA	Q6e4h7	petromyzon	1071	159.5	5.1	187	2	O6E4I5_PETMA	O6e4i5	petromyzon
999	163.5	5.2	362	2	Q502F2_BRARE	Q502f2	brachydanio	1072	159.5	5.1	235	2	O4G1I5_EPTST	O4g1i5	eptatretus
1000	163.5	5.2	370	2	Q9DE04_ORENI	Q9de04	oreochromis	1073	159.5	5.1	412	2	Q5MIQ1_AEDAL	Q5miq1	aedes albop
1001	163.5	5.2	582	2	Q5RSR1_PONPY	Q5rsr1	pongo pygma	1074	159.5	5.1	494	2	Q9LHF1_ARATH	Q9lhf1	arabidopsis
1002	163.5	5.2	671	2	Q53GZ4_HUMAN	Q53gz4	homo sapien	1075	159.5	5.1	520	1	AMGO2_RAT	Q7tnj4	rattus norv
1003	163.5	5.2	786	2	O48809_ARATH	O48809	arabidopsis	1076	159.5	5.1	636	2	Q8SQH3_CANFA	Q8sqh3	canis famil
1004	163	5.2	359	2	Q9DE03_ORENI	Q9de03	oreochromis	1077	159.5	5.1	722	2	O4KMG2_HUMAN	O4kmg2	homo sapien
1005	163	5.2	452	2	Q4RQB6_TETNG	Q4rqb6	tetraodon n	1078	159.5	5.1	1112	2	O64486_ARATH	O64486	arabidopsis
1006	163	5.2	501	2	Q6ZHB5_ORYSA	Q6zhb5	oryza sativ	1079	159	5.1	257	1	LRR3_RAT	P59035	rattus norv
1007	163	5.2	524	2	Q8R378_MOUSE	Q8r378	mus musculus	1080	159	5.1	524	1	LRR3_HUMAN	Q90tt6	homo sapien
1008	163	5.2	582	1	SHOC2_MOUSE	O88520	mus musculus	1081	159	5.1	524	2	Q5TGN3_HUMAN	Q5tgn3	homo sapien
1009	163	5.2	929	2	Q6P9N3_MOUSE	Q6p9n3	mus musculus	1082	159	5.1	543	2	Q8S7M7_ORYSA	Q8s7m7	oryza sativ
1010	163	5.2	933	2	Q9BJD5_STRPU	Q9bjd5	strongyloce	1083	159	5.1	550	1	LG12_MOUSE	Q8k4z0	mus musculus
1011	163	5.2	961	2	Q76CT7_PAROL	Q76ct7	paralichthy	1084	159	5.1	626	2	Q9NDD1_LEITR	Q9ndd1	leishmania
1012	163	5.2	961	2	Q76CT9_PAROL	Q76ct9	paralichthy	1085	159	5.1	671	2	Q60YZ3_CABER	Q60yz3	caenorhabdi
1013	163	5.2	1221	2	Q9BIW9_CABEL	Q9biw9	caenorhabdi	1086	159	5.1	695	2	Q93539_CABEL	Q93539	caenorhabdi
1014	163	5.2	1612	1	LAP4_MOUSE	Q80u72	mus musculus	1087	159	5.1	964	2	O86U22_HUMAN	O86u22	homo sapien
1015	162.5	5.2	283	2	Q9V4Z8_DROME	Q9v4z8	drosophila	1088	159	5.1	984	1	RIN3_HUMAN	Q86u22	homo sapien
1016	162.5	5.2	375	2	O5XIH1_RAT	O5xih1	rattus norv	1089	159	5.1	985	2	O76LB3_HUMAN	Q76lb3	homo sapien
1017	162.5	5.2	452	2	O8FL18_LEPIN	O8fl18	leptospora	1090	159	5.1	1119	2	O8ZOH2_ANASP	O8zoh2	anabaena sp
1018	162.5	5.2	494	2	Q9VEK6_DROME	Q9vek6	drosophila	1091	158.5	5.1	163	2	Q8E4E4_PETMA	Q8e4e4	petromyzon
1019	162.5	5.2	527	2	Q8PFB5_DROME	Q8pfb5	drosophila	1092	158.5	5.1	166	2	Q6E4B6_PETMA	Q6e4b6	petromyzon
1020	162.5	5.2	641	2	Q8MQM0_DROME	Q8mqm0	drosophila	1093	158.5	5.1	242	2	Q4SSH2_TETNG	Q4ssh2	tetraodon n
1021	162.5	5.2	700	2	Q4R6H5_MACFA	Q4r6h5	macaca fasc	1094	158.5	5.1	371	2	Q4T5R8_TETNG	Q4t5r8	tetraodon n
1022	162.5	5.2	1045	2	Q5H717_FUGRU	Q5h717	fugu rubrip	1095	158.5	5.1	417	2	O15828_LEICH	O15828	leishmania
1023	162	5.2	234	2	O4GLH3_EPTST	Q4glh3	eptatretus	1096	158.5	5.1	656	2	O19312_CAEEL	O19312	caenorhabdi
1024	162	5.2	242	2	Q9UG10_HUMAN	Q9ug10	homo sapien	1097	158.5	5.1	738	2	Q93373_CABEL	Q93373	caenorhabdi
1025	162	5.2	375	2	Q7QI18_ANOGA	Q7qi18	anopheles g	1098	158.5	5.1	943	2	Q4S133_TETNG	Q4s133	tetraodon n
1026	162	5.2	612	2	Q7Z5L7_HUMAN	Q7z5l7	homo sapien	1099	158.5	5.1	953	2	Q9V701_DROME	Q9v701	drosophila
1027	162	5.2	643	2	Q6UXL8_HUMAN	Q6uxl8	homo sapien	1100	158.5	5.1	1007	2	Q8MQU9_AEDAE	Q8mqu9	aedes aegypt
1028	162	5.2	642	2	O5VVZ2_HUMAN	O5vvz2	homo sapien	1101	158.5	5.1	1032	1	TLR8_MOUSE	P58682	mus musculus
1029	162	5.2	649	2	O8C2M4_MOUSE	O8c2m4	mus musculus	1102	158.5	5.1	1061	2	O655V6_ORYSA	O655v6	oryza sativ
1030	162	5.2	661	2	Q6PIR3_HUMAN	Q6pir3	homo sapien	1103	158.5	5.1	1123	2	Q65XS7_ORYSA	Q65xs7	oryza sativ
1031	162	5.2	661	2	Q5VVZ3_HUMAN	Q5vvz3	homo sapien	1104	158.5	5.1	1181	2	Q7ZZ35_BRARE	Q7zz35	brachydanio
1032	161.5	5.2	942	2	Q7QIS8_ANOGA	Q7qi18	anopheles g	1105	158.5	5.1	1202	1	CSK12_HUMAN	Q8wx0	homo sapien
1033	162	5.2	1040	2	Q6Z8Y3_ORYSA	Q6z8y3	oryza sativ	1106	158.5	5.1	1300	2	Q9NKD6_DROME	Q9nkD6	drosophila
1034	161.5	5.2	259	2	Q7QHK8_ANOGA	Q7qhk8	anopheles g	1107	158	5.0	239	2	O4KP19_9PETR	O4kp19	ichthyomyzo
1035	161.5	5.2	268	2	O4KP17_9PETR	O4kp17	ichthyomyzo	1108	158	5.0	249	2	O4KP07_LAMAP	O4kp07	lampetra ap
1036	161.5	5.2	351	2	Q5KT50_XENLA	Q5kt50	xenopus lae	1109	158	5.0	317	2	O6EB32_HUMAN	O6eb32	homo sapien
1037	161.5	5.2	507	2	Q9N3F2_CABEL	Q9njf2	caenorhabdi	1110	158	5.0	352	1	KERA_HUMAN	O60938	homo sapien
1038	161.5	5.2	519	2	Q7QI16_ANOGA	Q7qi16	anopheles g	1111	158	5.0	377	2	Q72U33_LEPIC	Q72u33	leptospora
1039	161.5	5.2	841	1	TLR4_BOVIN	Q9gl65	bos taurus	1112	158	5.0	510	2	Q9N1R8_DICDI	Q9n1r8	dictyosteli
1040	161.5	5.2	841	2	O6WCD4_BOVIN	O6wcd4	bos taurus	1113	158	5.0	531	2	O5TW51_ANOGA	O5tw51	anopheles g
1041	161.5	5.2	841	2	O6WCD5_BOVIN	O6wcd5	bos taurus	1114	158	5.0	677	2	O5XPV7_ICTPU	O5xpV7	ictalurus p
1042	161.5	5.2	841	2	Q8SQS5_BOVIN	Q8sq55	bos taurus	1115	158	5.0	741	2	Q9VJA9_DROME	Q9vja9	drosophila
1043	161.5	5.2	1193	2	Q4SL20_TETNG	Q4sl20	tetraodon n	1116	158	5.0	838	2	Q4SWS3_TETNG	Q4sws3	tetraodon n
1044	161.5	5.2	1270	2	Q5RK15_RAT	Q5rk15	rattus norv	1117	158	5.0	879	2	Q68C13_ONCMY	Q68c13	oncorhynch
1045	161	5.1	397	2	Q7QF88_ANOGA	Q7qf88	anopheles g	1118	158	5.0	909	2	Q6ZRC2_HUMAN	Q6zrc2	homo sapien
1046	161	5.1	558	2	Q8MPP6_CABEL	Q8mpp6	caenorhabdi	1119	158	5.0	1032	2	O56R09_AOTNA	O56r09	aotus nancy
1047	161	5.1	559	2	Q22875_CABEL	Q22875	caenorhabdi	1120	158	5.0	5703	1	MUC5B_HUMAN	O9hc84	homo sapien
1048	161	5.1	586	2	Q93377_CABEL	Q93377	caenorhabdi	1121	157.5	5.0	163	2	O6E4I4_PETMA	Q6e4i4	petromyzon
1049	161	5.1	682	1	CONN_DROME	Q01819	drosophila	1122	157.5	5.0	224	2	Q9DE01_BRARE	Q9de01	brachydanio
1050	161	5.1	691	2	Q6AWM0_DROME	Q6awm0	drosophila	1123	157.5	5.0	272	2	Q7KWF0_DROME	Q7kwf0	drosophila
1051	161	5.1	861	2	Q9SLS3_TOBAC	Q9sls3	nicotiana t	1124	157.5	5.0	276	2	O7PSP4_ANOGA	O7psp4	anopheles g
1052	161	5.1	905	2	Q7TN18_RAT	Q7tni8	rattus norv	1125	157.5	5.0	396	2	O5DZ80_VIBF1	O5dz80	vibrio fioc
1053	161	5.1	945	2	Q801F9_CARAU	Q801f9	carassius a	1126	157.5	5.0	655	2	Q4RW74_TETNG	Q4rw74	tetraodon n

1127	157.5	5.0	861	2	Q50TQ5_ENTHI	Q50tcq5	entamoeba h	1200	154.5	4.9	2461	2	Q56D06_HUMAN	Q56d06	homo sapien
1128	157.5	5.0	1102	2	Q4RZY0_TETNG	Q4rzy0	tetraodon n	1201	154.5	4.9	2517	1	NCOR2_HUMAN	Q85x16	h nuclear r
1129	157.5	5.0	2657	2	Q4S189_TETNG	Q4s189	tetraodon n	1202	154	4.9	399	2	Q8STX6_ENCCU	Q8stx6	encephalic
1130	157	5.0	266	2	Q7Q1P7_ANOGA	Q7q1p7	anopheles g	1203	154	4.9	458	2	Q9VU13_DROME	Q9vul3	drosophila
1131	157	5.0	273	2	Q9NUU4_HUMAN	Q9nuu4	homo sapien	1204	154	4.9	491	2	Q6KAP0_MOUSE	Q6kap0	mus musculus
1132	157	5.0	377	2	Q8F119_LEPIN	Q8f119	leptospiira	1205	154	4.9	530	2	P97830_RAT	P97830	rattus norv
1133	157	5.0	444	2	Q9HSH8_HUMAN	Q9hsh8	homo sapien	1206	154	4.9	584	2	Q49751_ARATH	Q49751	arabidopsis
1134	157	5.0	592	2	Q7L236_HUMAN	Q7l236	homo sapien	1207	154	4.9	584	2	Q8L722_ARATH	Q8l722	arabidopsis
1135	157	5.0	613	2	Q940E8_MAIZE	Q940e8	zea mays [m	1208	154	4.9	812	2	Q9VFY9_DROME	Q9vfy9	drosophila
1136	157	5.0	622	2	Q8N3B0_HUMAN	Q8n3b0	homo sapien	1209	154	4.9	825	2	Q63U08_BURPS	Q63u08	burkholderi
1137	157	5.0	680	1	LRCH4_MOUSE	Q921g6	mus musculus	1210	154	4.9	953	2	Q8VYG7_ARATH	Q8v yg7	arabidopsis
1138	157	5.0	796	2	Q6NSJ5_HUMAN	Q6nsj5	homo sapien	1211	154	4.9	965	2	QSH724_FUGRU	Qsh724	fugu rubrip
1139	157	5.0	903	2	Q6LW15_BRARE	Q6lw15	brachydanio	1212	154	4.9	1845	2	Q8OUA8_MOUSE	Q8oua8	mus musculus
1140	157	5.0	1032	2	Q5I2M6_RAT	Q5i2m6	rattus norv	1213	153.5	4.9	163	2	Q6E4L8_PETMA	Q6e4l8	petromyzon
1141	157	5.0	1032	2	Q6V1S0_RAT	Q6v1s0	rattus norv	1214	153.5	4.9	166	2	Q6E4G9_PETMA	Q6e4g9	petromyzon
1142	156.5	5.0	305	2	Q50Q05_ENTHI	Q50q05	entamoeba h	1215	153.5	4.9	246	2	Q4KP02_LAMAP	Q4kp02	lampetra ap
1143	156.5	5.0	360	1	PGS2_RABIT	Q28888	oryctolagus	1216	153.5	4.9	366	2	Q5R858_PONPY	Q5r858	pongo pygma
1144	156.5	5.0	376	1	PMOD_HUMAN	Q06828	homo sapien	1217	153.5	4.9	389	2	Q4RHN9_TETNG	Q4rhn9	tetraodon n
1145	156.5	5.0	428	2	Q9VDD4_DROME	Q9vdd4	drosophila	1218	153.5	4.9	403	2	Q96CX6_HUMAN	Q96cx6	homo sapien
1146	156.5	5.0	487	2	Q7Q087_ANOGA	Q7q087	anopheles g	1219	153.5	4.9	526	2	Q5BL36_BRARE	Q5bl36	brachydanio
1147	156.5	5.0	505	2	Q4RVS9_TETNG	Q4rvs9	tetraodon n	1220	153.5	4.9	655	2	Q9FBR7_STRCO	Q9fbr7	streptomyce
1148	156.5	5.0	524	2	Q6AXP5_RAT	Q6axp5	rattus norv	1221	153.5	4.9	685	2	Q72TH0_LPIC	Q72th0	leptospiira
1149	156.5	5.0	551	2	Q5ZB68_ORYSA	Q5zb68	oryza sativ	1222	153.5	4.9	802	2	Q8F1V0_LEPIN	Q8f1v0	leptospiira
1150	156.5	5.0	711	2	Q9SPM1_LYCES	Q9spm1	lycopersico	1223	153.5	4.9	802	2	Q8L4U4_ORYSA	Q8l4u4	oryza sativ
1151	156.5	5.0	887	1	UFO_HUMAN	P30530	homo sapien	1224	153.5	4.9	864	2	Q8LPG4_ARATH	Q8lpg4	arabidopsis
1152	156.5	5.0	980	2	Q9ZU10_ARATH	Q9zu10	arabidopsis	1225	153.5	4.9	864	2	Q9T033_ARATH	Q9t033	arabidopsis
1153	156.5	5.0	1179	2	Q7PWD3_ANOGA	Q7pwd3	anopheles g	1226	153.5	4.9	894	2	Q8N5L2_HUMAN	Q8n5l2	homo sapien
1154	156.5	5.0	1301	2	Q9VZ81_DROME	Q9vz81	drosophila	1227	153.5	4.9	940	2	Q4RGH3_TETNG	Q4rgh3	tetraodon n
1155	156.5	5.0	1766	2	Q6XHA8_DICDI	Q6xha8	dictyosteli	1228	153.5	4.9	987	2	Q53MD2_ORYSA	Q53md2	oryza sativ
1156	156.5	5.0	1867	2	Q54M77_DICDI	Q54m77	dictyosteli	1229	153.5	4.9	1032	1	TLR9_HUMAN	Q9nr96	homo sapien
1157	156	5.0	163	2	Q6E4D5_PETMA	Q6e4d5	petromyzon	1230	153.5	4.9	1041	2	Q9F1I5_ARATH	Q9f1i5	arabidopsis
1158	156	5.0	163	2	Q6E4F5_PETMA	Q6e4f5	petromyzon	1231	153.5	4.9	1110	2	Q9F177_ARATH	Q9f177	arabidopsis
1159	156	5.0	257	1	LRRC3_HUMAN	Q9b171	rattus norv	1232	153.5	4.9	1121	2	Q942F3_ORYSA	Q942f3	oryza sativ
1160	156	5.0	354	1	PGS2_RAT	Q01129	rattus norv	1233	153.5	4.9	1388	2	Q4RIV6_TETNG	Q4riv6	tetraodon n
1161	156	5.0	422	2	Q4RH13_TETNG	Q4rh13	tetraodon n	1234	153.5	4.9	3247	2	Q6S553_9ALPH	Q6s553	bovine herp
1162	156	5.0	469	2	Q9WL28_DROME	Q9wl28	drosophila	1235	153.5	4.9	3247	2	Q77CD4_9ALPH	Q77cd4	bovine herp
1163	156	5.0	547	2	Q4QI16_LEIMA	Q4q116	leishmania	1236	153	4.9	367	2	Q6GLE8_XENTR	Q6gle8	xenopus tro
1164	156	5.0	552	2	Q8K375_MOUSE	Q8k375	mus musculus	1237	153	4.9	529	2	Q5F4C4_CHICK	Q5f4c4	gallus gall
1165	156	5.0	575	2	Q571F2_MOUSE	Q571f2	mus musculus	1238	153	4.9	548	2	Q4V8C9_RAT	Q4v8c9	rattus norv
1166	156	5.0	594	2	Q9U3A0_CAEEL	Q9u3a0	caenorhabdi	1239	153	4.9	581	2	Q9D5O5_MOUSE	Q9d5o5	m mus muscu
1167	156	5.0	643	2	Q6Q148_RAT	Q6q148	rattus norv	1240	153	4.9	590	2	Q9D2F4_MOUSE	Q9d2f4	h mus muscu
1168	156	5.0	704	2	Q4QK11_LEIMA	Q4qk11	leishmania	1241	153	4.9	699	1	VGLG_HV2H	V13290	human herpe
1169	156	5.0	940	2	Q8T753_BRAFL	Q8t753	branchiosto	1242	153	4.9	720	2	Q6PQA5_SPAAU	Q6pqa5	sparus aua
1170	156	5.0	953	2	Q617Q9_CAEER	Q617q9	caenorhabdi	1243	153	4.9	1840	2	Q9ULI4_HUMAN	Q9uli4	homo sapien
1171	156	5.0	1039	2	Q6GBL1_DROME	Q6gb11	drosophila	1244	153	4.9	2042	1	MDC1_PIG	Q76718	sus scrofa
1172	155.5	5.0	332	2	Q6C2U8_YARLI	Q6c2u8	yarrowia li	1245	152.5	4.9	163	2	Q5E4F3_PETMA	Q5e4f3	petromyzon
1173	155.5	5.0	338	2	Q6VEX8_CHICK	Q6vex8	gallus gall	1246	152.5	4.9	370	2	Q5R9V7_PONPY	Q5r9v7	pongo pygma
1174	155.5	5.0	367	2	Q8BK43_MOUSE	Q8bk43	mus musculus	1247	152.5	4.9	372	2	Q5VZS8_HUMAN	Q5vzs8	homo sapien
1175	155.5	5.0	664	2	Q5EWY6_CTEID	Q5ewy6	ctenopharyn	1248	152.5	4.9	550	2	Q7PT66_ANOGA	Q7pt66	anopheles g
1176	155.5	5.0	980	2	Q8QWA0_MOUSE	Q8qwa0	mus musculus	1249	152.5	4.9	577	2	Q8AVI4_XENLA	Q8avi4	xenopus lae
1177	155.5	5.0	1102	2	Q8KC98_CHLTE	Q8kc98	chlorobium	1250	152.5	4.9	581	2	Q9AN90_BRAJA	Q9an90	bradyrhizob
1178	155.5	5.0	1135	2	Q8ARP6_ARATH	Q8arp6	arabidopsis	1251	152.5	4.9	585	2	Q89TL5_BRAJA	Q89tl5	bradyrhizob
1179	155.5	5.0	1285	1	CRUM2_HUMAN	Q51j48	homo sapien	1252	152.5	4.9	849	1	LAP1_DROME	Q9v780	drosophila
1180	155.5	5.0	1334	2	Q9RRR9_STRCO	Q9rrr9	streptomyce	1253	152.5	4.9	1047	2	Q5H719_FUGRU	Q5h719	fugu rubrip
1181	155	4.9	347	2	Q9DE00_PETMA	Q9de00	petromyzon	1254	152.5	4.9	1109	2	Q8H4J0_ORYSA	Q8h4j0	oryza sativ
1182	155	4.9	504	1	AMGQ3_HUMAN	Q86wk7	homo sapien	1255	152.5	4.9	1287	2	Q5TMV4_AMOGA	Q5tmv4	anopheles g
1183	155	4.9	576	2	Q6ZBP4_ORYSA	Q6zbp4	oryza sativ	1256	152.5	4.9	1295	2	Q8T0X1_BOMMO	Q8t0x1	bombyx mori
1184	155	4.9	719	2	Q8VJQ6_MYCTU	Q8vjq6	mycobacteri	1257	152.5	4.9	1356	2	Q8WRE2_ANOGA	Q8wre2	anopheles g
1185	155	4.9	825	2	Q6ZJU6_BURNA	Q6zju6	burkholderi	1258	152.5	4.9	1817	2	Q4WMC5_ASFFU	Q4wmc5	aspergillus
1186	155	4.9	961	2	P90920_CAEEL	P90920	caenorhabdi	1259	152.5	4.9	3288	2	Q7T5D9_CHV1	Q7t5d9	cercopithe
1187	155	4.9	1041	1	TLR8_HUMAN	Q9nr97	homo sapien	1260	152	4.8	443	1	LRC17_MOUSE	Q9cxd9	mus musculus
1188	154.5	4.9	219	2	Q9QWZ2_CHICK	Q9qwz2	gallus gall	1261	152	4.8	562	2	Q9M7W9_ARATH	Q9m7w9	arabidopsis
1189	154.5	4.9	246	2	Q4KP18_9PETR	Q4kp18	ichthyomyzo	1262	152	4.8	682	2	Q5JN60_ORYSA	Q5jn60	oryza sativ
1190	154.5	4.9	376	2	Q8IV47_HUMAN	Q8iv47	homo sapien	1263	152	4.8	776	2	Q8R2K3_ARATH	Q8r2k3	arabidopsis
1191	154.5	4.9	524	1	LRRC1_MOUSE	Q8ovq1	mus musculus	1264	152	4.8	786	1	TLR1_HUMAN	Q15399	homo sapien
1192	154.5	4.9	548	2	Q9VJUI_DROME	Q9vjui	drosophila	1265	152	4.8	786	2	Q6F164_HUMAN	Q6f164	homo sapien
1193	154.5	4.9	606	2	Q57IM3_MOUSE	Q57im3	mus musculus	1266	152	4.8	786	2	Q5FWG5_HUMAN	Q5fwg5	homo sapien
1194	154.5	4.9	631	2	Q8TN14_METAC	Q8tn14	methanosarc	1267	152	4.8	796	1	TLR6_HUMAN	Q9v2c9	homo sapien
1195	154.5	4.9	1013	2	Q9M0G7_ARATH	Q9m0g7	arabidopsis	1268	152	4.8	863	2	Q4R6F0_MACFA	Q4r6f0	macaca faec
1196	154.5	4.9	1109	2	Q6YT77_ORYSA	Q6yt77	oryza sativ	1269	151.5	4.8	347	2	Q9D9Q0_MOUSE	Q9d9q0	mus musculus
1197	154.5	4.9	1143	2	Q9SUB9_ARATH	Q9sub9	arabidopsis	1270	151.5	4.8	507	2	Q6IX12_CAEER	Q6ix12	caenorhabdi
1198	154.5	4.9	1192	1	EXS_ARATH	Q9lyn8	arabidopsis	1271	151.5	4.8	623	2	Q7Q090_ANOGA	Q7q090	anopheles g
1199	154.5	4.9	1961	2	Q6MG89_RAT	Q6mg89	rattus norv	1272	151.5	4.8	710	2	Q5TR39_ANOGA	Q5tr39	anopheles g

1273	151.5	4.8	855	2	Q8L3Y5_SOYBN	Q8L3Y5 glycine max
1274	151.5	4.8	997	2	Q6K7X5_ORYSA	Q6K7X5 oryza sativ
1275	151.5	4.8	998	2	Q4W9M1_ASFPU	Q4W9M1 aspergillus
1276	151.5	4.8	1109	2	Q84ZJ8_ORYSA	Q84ZJ8 oryza sativ
1277	151.5	4.8	1152	2	Q7PFC4_ANOGA	Q7PFC4 anopheles g
1278	151.5	4.8	1152	2	Q8WRE5_ANOGA	Q8WRE5 anopheles g
1279	151.5	4.8	1775	2	Q54811_DICDI	Q54811 dictyosteli
1280	151	4.8	163	2	Q6E4H9_PETMA	Q6E4H9 petromyzon
1281	151	4.8	399	2	Q8BM45_MOUSE	Q8BM45 m mus muscu
1282	151	4.8	508	2	Q5OZ76_ENTHI	Q5OZ76 entamoeba h
1283	151	4.8	530	2	Q08934_MOUSE	Q08934 mus musculu
1284	151	4.8	540	2	Q6V6S6_DROSI	Q6V6S6 drosophila
1285	151	4.8	540	2	P93666_HELAN	P93666 helianthus
1286	151	4.8	541	2	Q6V6S8_DROSI	Q6V6S8 drosophila
1287	151	4.8	541	2	Q6V6S9_DROSI	Q6V6S9 drosophila
1288	151	4.8	541	2	Q6V6T0_DROSI	Q6V6T0 drosophila
1289	151	4.8	581	2	Q04143_SILLA	Q04143 silene lati
1290	151	4.8	784	2	Q6YGU2_RAT	Q6YGU2 rattus norv
1291	151	4.8	793	2	Q704V6_BOVIN	Q704V6 bos taurus
1292	151	4.8	793	2	Q706D2_BOVIN	Q706D2 bos taurus
1293	151	4.8	835	1	TLR4_MOUSE	TLR4 mouse
1294	151	4.8	835	2	Q5RG74_MOUSE	Q5RG74 mus musculu
1295	151	4.8	947	2	Q8RUT5_ORYSA	Q8RUT5 oryza sativ
1296	151	4.8	1030	2	Q8H037_ORYSA	Q8H037 oryza sativ
1297	151	4.8	1385	2	Q9V8Z5_DROME	Q9V8Z5 drosophila
1298	151	4.8	1389	2	Q24591_DROME	Q24591 drosophila
1299	150.5	4.8	289	2	Q8F3F4_LEPIN	Q8F3F4 leptospira
1300	150.5	4.8	329	2	Q8F115_LEPIN	Q8F115 leptospira
1301	150.5	4.8	408	2	Q8F212_LEPIN	Q8F212 leptospira
1302	150.5	4.8	413	2	Q72TC4_LEPIC	Q72TC4 leptospira
1303	150.5	4.8	423	1	OMD_RAT	OMD rat
1304	150.5	4.8	537	2	Q9C769_ARATH	Q9C769 arabidopsis
1305	150.5	4.8	641	2	Q4TBJ8_TETNG	Q4TBJ8 tetraodon n
1306	150.5	4.8	648	2	Q8BU93_MOUSE	Q8BU93 m mus muscu
1307	150.5	4.8	685	2	Q6AXL3_BRARE	Q6AXL3 brachydanio
1308	150.5	4.8	695	1	FSHR_HUMAN	FSHR human
1309	150.5	4.8	695	2	Q4ORJ3_HUMAN	Q4ORJ3 homo sapien
1310	150.5	4.8	818	2	Q76CU0_PAROL	Q76CU0 paralichthy
1311	150.5	4.8	871	2	Q5H726_FUGRU	Q5H726 fugu rubrip
1312	150.5	4.8	1107	2	Q8BKP3_MOUSE	Q8BKP3 m mus muscu
1313	150.5	4.8	1109	1	RPK1_IPONI	RPK1 ipomoea nil
1314	150.5	4.8	1140	2	Q9LR04_ARATH	Q9LR04 arabidopsis
1315	150.5	4.8	1149	2	Q6GOR9_MOUSE	Q6GOR9 mus musculu
1316	150.5	4.8	1461	2	Q9AH87_ORYSA	Q9AH87 oryza sativ
1317	150.5	4.8	1702	2	Q7FS33_ANOGA	Q7FS33 anopheles g
1318	150.5	4.8	1898	2	Q6ZP14_MOUSE	Q6ZP14 mus musculu
1319	150.5	4.8	1944	2	Q4S1G7_TETNG	Q4S1G7 tetraodon n
1320	150	4.8	163	2	Q6E4E8_PETMA	Q6E4E8 macaca fasc
1321	150	4.8	239	2	Q4KP08_LAMAP	Q4KP08 lampetra ap
1322	150	4.8	259	1	LRC3B_HUMAN	LRC3B homo sapien
1323	150	4.8	259	1	Q8C3B_MOUSE	Q8C3B mus musculu
1324	150	4.8	259	2	Q5M8T0_HUMAN	Q5M8T0 homo sapien
1325	150	4.8	259	2	Q543Z7_MOUSE	Q543Z7 mus musculu
1326	150	4.8	272	1	PGS1_PIG	PGS1 sus scrofa
1327	150	4.8	305	2	Q9N0Z8_MACFA	Q9N0Z8 macaca fasc
1328	150	4.8	342	2	Q4V9E0_BRARE	Q4V9E0 brachydanio
1329	150	4.8	348	2	Q756S8_ASHGO	Q756S8 ashbya goss
1330	150	4.8	367	2	Q86X40_HUMAN	Q86X40 homo sapien
1331	150	4.8	584	2	Q49750_ARATH	Q49750 arabidopsis
1332	150	4.8	594	2	Q4SDI8_TETNG	Q4SDI8 tetraodon n
1333	150	4.8	652	2	Q8GUM9_ARATH	Q8GUM9 arabidopsis
1334	150	4.8	796	2	Q5SH1C_PIG	Q5SH1C sus scrofa
1335	150	4.8	796	2	Q76L23_PIG	Q76L23 pig
1336	150	4.8	802	2	Q8LFN2_ARATH	Q8LFN2 sus scrofa
1337	150	4.8	803	2	Q9SRV4_ARATH	Q9SRV4 arabidopsis
1338	150	4.8	1294	2	Q8ZV77_ORYSA	Q8ZV77 oryza sativ
1339	150	4.8	1305	1	TCGAP_MOUSE	TCGAP mus musculu
1340	150	4.8	1315	1	CHAO_DROME	CHAO drosophila
1341	149.5	4.8	98	2	Q9XG3_CHICK	Q9XG3 gallus gall
1342	149.5	4.8	163	2	Q6E4E9_PETMA	Q6E4E9 petromyzon
1343	149.5	4.8	164	2	Q6E4G8_PETMA	Q6E4G8 petromyzon
1344	149.5	4.8	167	2	Q6E4I1_PETMA	Q6E4I1 petromyzon
1345	149.5	4.8	224	2	Q44086_CABEL	Q44086 caenorhabdi

1346	149.5	4.8	542	2	Q5V4C6_DROYA	Q5V4C6 drosophila
1347	149.5	4.8	657	2	Q6L589_ORYSA	Q6L589 oryza sativ
1348	149.5	4.8	696	2	Q8DGF5_CYNPY	Q8DGF5 cynops pyrr
1349	149.5	4.8	894	2	Q8GYR8_ARATH	Q8GYR8 arabidopsis
1350	149.5	4.8	957	2	Q9SRL2_ARATH	Q9SRL2 arabidopsis
1351	149.5	4.8	1056	2	Q7XFM6_ORYSA	Q7XFM6 oryza sativ
1352	149.5	4.8	1056	2	Q8S7A6_ORYSA	Q8S7A6 oryza sativ
1353	149.5	4.8	1469	2	Q51AW9_ENTHI	Q51AW9 entamoeba h
1354	149.5	4.8	1791	2	Q4P4A9_USTMA	Q4P4A9 ustilago ma
1355	149	4.8	295	2	Q6E4D3_PETMA	Q6E4D3 petromyzon
1356	149	4.8	295	2	Q86DD0_CABEL	Q86DD0 caenorhabdi
1357	149	4.8	310	2	Q86S81_CABEL	Q86S81 caenorhabdi
1358	149	4.8	341	2	Q9NSD7_CABEL	Q9NSD7 caenorhabdi
1359	149	4.8	366	2	Q7QH02_ANOGA	Q7QH02 anopheles g
1360	149	4.8	375	2	Q9N4Z5_CABEL	Q9N4Z5 caenorhabdi
1361	149	4.8	421	2	Q7PNQ0_ANOGA	Q7PNQ0 anopheles g
1362	149	4.8	437	2	Q7Q6S9_ANOGA	Q7Q6S9 anopheles g
1363	149	4.8	471	2	Q9LRV8_ARATH	Q9LRV8 arabidopsis
1364	149	4.8	763	2	Q4Q5O5_LEIMA	Q4Q5O5 leishmania
1365	149	4.8	784	1	TLR2_CRIGR	TLR2 cricetus
1366	149	4.8	927	2	Q8NS37_HUMAN	Q8NS37 homo sapien
1367	149	4.8	972	2	Q5AXH5_EMENI	Q5AXH5 aspergillus
1368	149	4.8	1025	2	Q4Q640_ORYSA	Q4Q640 oryza sativ
1369	149	4.8	1025	2	Q7DMC2_ORYLO	Q7DMC2 oryza longi
1370	149	4.8	1143	1	BRL2_ARATH	BRL2 arabidopsis
1371	149	4.8	1164	2	Q53JZ9_ORYSA	Q53JZ9 oryza sativ
1372	149	4.8	1504	2	Q9UES6_HUMAN	Q9UES6 homo sapien
1373	149	4.8	1504	2	Q6P1B4_HUMAN	Q6P1B4 homo sapien
1374	149	4.8	1504	2	Q7Z2X6_HUMAN	Q7Z2X6 homo sapien
1375	149	4.8	1504	2	Q6PGP3_HUMAN	Q6PGP3 homo sapien
1376	149	4.8	1522	2	Q15069_HUMAN	Q15069 homo sapien
1377	149	4.8	1528	2	Q9Y211_HUMAN	Q9Y211 homo sapien
1378	149	4.8	1874	2	Q75F93_ASHGO	Q75F93 ashbya goss
1379	149	4.8	2357	2	Q869S1_DICDI	Q869S1 dictyosteli
1380	149	4.8	2357	2	Q9U1M8_DICDI	Q9U1M8 dictyosteli
1381	148.5	4.7	163	2	Q6E4F7_PETMA	Q6E4F7 petromyzon
1382	148.5	4.7	215	2	Q91VH8_MOUSE	Q91VH8 mus musculu
1383	148.5	4.7	232	2	Q5T508_HUMAN	Q5T508 homo sapien
1384	148.5	4.7	321	2	Q6X8F9_BOVIN	Q6X8F9 bos taurus
1385	148.5	4.7	375	1	FNOD_BOVIN	FNOD bos taurus
1386	148.5	4.7	376	1	FNOD_RAT	FNOD rattus norv
1387	148.5	4.7	516	2	Q4T9I8_TETNG	Q4T9I8 tetraodon n
1388	148.5	4.7	610	2	Q21604_CABEL	Q21604 caenorhabdi
1389	148.5	4.7	646	2	Q8PQD3_XANAC	Q8PQD3 xanthomonas
1390	148.5	4.7	680	2	Q93374_CABEL	Q93374 caenorhabdi
1391	148.5	4.7	687	2	Q61PG2_CABBR	Q61PG2 caenorhabdi
1392	148.5	4.7	695	1	FSHR_MACFA	FSHR macaca fasc
1393	148.5	4.7	807	2	Q6GPJ8_XENLA	Q6GPJ8 xenopus lae
1394	148.5	4.7	890	2	Q9LQ11_ARATH	Q9LQ11 arabidopsis
1395	148.5	4.7	964	2	Q8VY77_ARATH	Q8VY77 arabidopsis
1396	148.5	4.7	964	2	Q9LY03_ARATH	Q9LY03 arabidopsis
1397	148.5	4.7	1013	2	Q96PY9_HUMAN	Q96PY9 homo sapien
1398	148.5	4.7	1016	2	Q9LRT1_ARATH	Q9LRT1 arabidopsis
1399	148.5	4.7	1099	2	Q8WX84_HUMAN	Q8WX84 homo sapien
1400	148.5	4.7	1115	1	GR101_LYMET	GR101 lymnaea ata
1401	148.5	4.7	1140	2	Q7S718_NEUCR	Q7S718 neurospora
1402	148.5	4.7	1279	2	Q4RJ85_TETNG	Q4RJ85 tetraodon n
1403	148	4.7	311	2	Q8F116_LEPIN	Q8F116 leptospira
1404	148	4.7	338	1	LUM_RAT	LUM rat
1405	148	4.7	449	2	Q4SR98_TETNG	Q4SR98 tetraodon n
1406	148	4.7	572	2	Q7S279_LEPIC	Q7S279 leptospira
1407	148	4.7	581	2	Q5O5F5_MOUSE	Q5O5F5 mus musculu
1408	148	4.7	592	2	Q4REF6_TETNG	Q4REF6 tetraodon n
1409	148	4.7	724	2	Q651V0_ORYSA	Q651V0 oryza sativ
1410	148	4.7	745	2	Q89X06_BRAJA	Q89X06 bradyrhizob
1411	148	4.7	811	2	Q59H15_PIG	Q59H15 sus scrofa
1412	148	4.7	811	2	Q4LDR6_PIG	Q4LDR6 sus scrofa
1413	148	4.7	915	2	Q5SMW5_ORYSA	Q5SMW5 oryza sativ
1414	148	4.7	1095	2	Q6URA2_9ROSA	Q6URA2 malus baccia
1415	148	4.7	1188	2	Q41805_WAIZE	Q41805 zea mays (m
1416	148	4.7	1964	1	NOTC4_MOUSE	P31695 mus musculu
1417	148	4.7	2143	2	Q75T35_GLOLA	Q75T35 glomerella
1418	147.5	4.7	163	2	Q6E4M8_PETMA	Q6E4M8 petromyzon

QY 1 MCSRVPLLLPLLLALLGPGVQCGSCGCSQPTVCTARQGTTPVPRDVPDVTGLVVF 60
Db 1 MCSRVPLLLPLLLALLGPGVQCGSCGCSQPTVCTARQGTTPVPRDVPDVTGLVVF 60
QY 61 ENGITMLDASSFAGLPGQLLDLSNQIASLRLPRLLLDLSHNSLLALEPGILDTANVE 120
Db 61 ENGITMLDASSFAGLPGQLLDLSNQIASLRLPRLLLDLSHNSLLALEPGILDTANVE 120
QY 121 ALRLAGLGLQDDEGLFSLRLNLHDLVDSDNQLERVPVIRGLRGLTRILAGNTRIAQL 180
Db 121 ALRLAGLGLQDDEGLFSLRLNLHDLVDSDNQLERVPVIRGLRGLTRILAGNTRIAQL 180
QY 181 REDLADLAALQELVDNLSLQALPGDLGSLPRLRLLAANPNPCVLSWFGPWVRE 240
Db 181 REDLADLAALQELVDNLSLQALPGDLGSLPRLRLLAANPNPCVLSWFGPWVRE 240
QY 241 SHVTLASPEETRCHFPKPNAGRLLELDYADFQCPATTTTATVPTTRPVPREPTALSSSL 300
Db 241 SHVTLASPEETRCHFPKPNAGRLLELDYADFQCPATTTTATVPTTRPVPREPTALSSSL 300
QY 301 APTWLSPTAPATEAPSPSTAPPTVGPVPOQDCPPSTCLNGTCHLGRHHLACLCPGEG 360
Db 301 APTWLSPTAPATEAPSPSTAPPTVGPVPOQDCPPSTCLNGTCHLGRHHLACLCPGEG 360
QY 361 FTGLYCESOMGOTRPSPTVTPRPRSLTLGIEPVSPSLRVGLQRYLQSSVOLRSILR 420
Db 361 FTGLYCESOMGOTRPSPTVTPRPRSLTLGIEPVSPSLRVGLQRYLQSSVOLRSILR 420
QY 421 LTYRNLSPGDKRLVTLRLPASLAETVTLQLRPNATYSVCVMPGLPGRVPEGEACGEAHT 480
Db 421 LTYRNLSPGDKRLVTLRLPASLAETVTLQLRPNATYSVCVMPGLPGRVPEGEACGEAHT 480
QY 481 PPAVSHNAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRGRAMAAAAQDKGV 540
Db 481 PPAVSHNAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRGRAMAAAAQDKGV 540
QY 541 GPGAGPLEEGVKVPLEPGPKATGEGGALPGSGCEVPLMGFGPGQLSPHAKPYI 598
Db 541 GPGAGPLEEGVKVPLEPGPKATGEGGALPGSGCEVPLMGFGPGQLSPHAKPYI 598

RESULT 2
Q6UXL4 HUMAN
AC Q6UXL4; HUMAN PRELIMINARY; PRT; 673 AA.
DT 05-JUL-2004 (TremBLrel. 27, Created)
DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)
DT 13-SEP-2005 (TremBLrel. 31, Last annotation update)
DE CSRV314 (Slit-like 2).
GN Name=SLIT2; ORFNames=UNQ314;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klinowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,
RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Placenta;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzly D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield V.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RG NIH MGC Project;
RL Submitted (A00-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY358299; AAQ88666.1; -; mRNA.
DR EMBL; BC068575; AAH68575.1; -; mRNA.
DR Ensembl; ENSG00000168140; Homo sapiens.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR Cterm.
DR InterPro; IPR003885; LRR cyst.
DR InterPro; IPR000372; LRR Nterm.
DR InterPro; IPR003591; LRR typ.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00560; LRR 1; 6.
DR Pfam; PF01462; LRRNT; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00365; LRR SD22; 4.
DR SMART; SM00369; LRR typ; 8.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00013; LRRNT; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS00853; FN3; 1.
SQ SEQUENCE 673 AA; 71655 MW; 4CDA391231D4BF8 CRC64;
Query Match 98.4%; Score 3083.5; DB 2; Length 673;
Best Local Similarity 98.7%; Pred. No. 1.1e-165; Mismatches 0; Indels 75; Gaps 1;
Matches 597; Conservative 1;
QY 1 MCSRVPLLLPLLLALLGPGVQCGSCGCSQPTVCTARQGTTPVPRDVPDVTGLVVF 60
Db 1 MCSRVPLLLPLLLALLGPGVQCGSCGCSQPTVCTARQGTTPVPRDVPDVTGLVVF 60
QY 61 ENGITMLDASSFAGLPGQLLDLSNQIASLRLPRLLLDLSHNSLLALEPGILDTANVE 120
Db 61 ENGITMLDASSFAGLPGQLLDLSNQIASLRLPRLLLDLSHNSLLALEPGILDTANVE 120
QY 121 ALRLAGLGLQDDEGLFSLRLNLHDLVDSDNQLERVPVIRGLRGLTRILAGNTRIAQL 180
Db 121 ALRLAGLGLQDDEGLFSLRLNLHDLVDSDNQLERVPVIRGLRGLTRILAGNTRIAQL 180
QY 181 REDLADLAALQELVDNLSLQALPGDLGSLPRLRLLAANPNPCVLSWFGPWVRE 240
Db 181 REDLADLAALQELVDNLSLQALPGDLGSLPRLRLLAANPNPCVLSWFGPWVRE 240
QY 241 SHVTLASPEETRCHFPKPNAGRLLELDYADFQCPATTTTATVPTTRPVPREPTALSSSL 300
Db 241 SHVTLASPEETRCHFPKPNAGRLLELDYADFQCPATTTTATVPTTRPVPREPTALSSSL 300
QY 301 APTWLSPTAPATEAPSPSTAPPTVGPVPOQDCPPSTCLNGTCHLGRHHLACLCPGEG 360
Db 301 APTWLSPTAPATEAPSPSTAPPTVGPVPOQDCPPSTCLNGTCHLGRHHLACLCPGEG 360
QY 361 FTGLYCESOMGOTRPSPTVTPRPRSLTLGIEPVSPSLRVGLQRYLQSSVOLRSILR 420
Db 361 FTGLYCESOMGOTRPSPTVTPRPRSLTLGIEPVSPSLRVGLQRYLQSSVOLRSILR 420
QY 421 LTYRNLSPGDKRLVTLRLPASLAETVTLQLRPNATYSVCVMPGLPGRVPEGEACGEAHT 480
Db 421 LTYRNLSPGDKRLVTLRLPASLAETVTLQLRPNATYSVCVMPGLPGRVPEGEACGEAHT 480
QY 481 PPAVSHNAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRGRAMAAAAQDKGV 540
Db 481 PPAVSHNAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRGRAMAAAAQDKGV 540
QY 541 GPGAGPLEEGVKVPLEPGPKATGEGGALPGSGCEVPLMGFGPGQLSPHAKPYI 598
Db 541 GPGAGPLEEGVKVPLEPGPKATGEGGALPGSGCEVPLMGFGPGQLSPHAKPYI 598

Db 181 LLALRPGILDTANVEALRIAGLGLQQLDEGLFRLRLNHLHDLDVSDNQLRVPVIRGLRG 240
Qy 166 LTRLRAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLGLFPRRLILAAARNPF 225
Db 241 LTRLRAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLGLFPRRLILAAARNPF 300
Qy 226 NCVCPLSWFGPWVRESHVTLASPEETRCHFPKPNAGRLLELDYADFGCPATTTATVPT 285
Db 301 NCVCPLSWFGPWVRESHVTLASPEETRCHFPKPNAGRLLELDYADFGCPATTTATVPT 360
Qy 286 TRPVREPTALSSSLAPTWSPTAPATEAPSPSTAPPTVGPVPOQDCPPSTCLNGGTC 345
Db 361 TRPVREPTALSSSLAPTWSPTAPATEAPSPSTAPPTVGPVPOQDCPPSTCLNGGTC 420
Qy 346 HLGTRHHLACLCEGFTGLYCESQMGQTRPSPTVTPRPSRLTLGIEPVSPSLRVGL 405
Db 421 HLGTRHHLACLCEGFTGLYCESQMGQTRPSPTVTPRPSRLTLGIEPVSPSLRVGL 480
Qy 406 QRYLOGSSVOLRLTYRNLSGPDKRLVTLRLPASLAETVTLQRPNATYSVCVMPGLP 465
Db 481 QRYLOGSSVOLRLTYRNLSGPDKRLVTLRLPASLAETVTLQRPNATYSVCVMPGLP 540
Qy 466 GRVPEGEACGEAHTPPAVHNSHAPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVR 525
Db 541 GRVPEGEACGEAHTPPAVHNSHAPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVR 600
Qy 526 RGRMAAAAQDKGVQFGAGPLEGKVKVPLEPGPKATGGGEALPSGSECEVPLMGFPF 585
Db 601 RGRMAAAAQDKGVQFGAGPLEGKVKVPLEPGPKATGGGEALPSGSECEVPLMGFPF 660
Qy 586 PGLQSPHLHAKPYI 598
Db 661 PGLQSPHLHAKPYI 673

RESULT 3
Q6EMK4 HUMAN
ID Q6EMK4 HUMAN PRELIMINARY; PRT; 673 AA.
AC Q6EMK4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Vasorin.
GN Name=SLITL2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15247411; DOI=10.1073/pnas.0404117101;
RA Ikeda Y., Imai Y., Kumagai H., Noseka T., Morikawa Y., Hiseoka T.,
RA Manabe I., Maemura K., Nakaoka T., Imamura T., Miyazono K., Komuro I.,
RA Nagai R., Kitamura T.;
RT "Vasorin, a transforming growth factor [beta]-binding protein
RT expressed in vascular smooth muscle cells, modulates the arterial
RT response to injury in vivo.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:10732-10737(2004).
DR EMBL; AY166584; AA027704.1; -; mRNA.
DR Ensembl; ENSG00000168140; Homo sapiens.
DR HGNC; HGNC:18517; SLITL2.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR003885; LRR_Cyst.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003591; LRR_Typ.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00041; fn3; 1.

DR Pfam; PF01463; LRRCT; 1.
DR Pfam; PF01462; LRRNT; 1.
DR Pfam; PF00560; LRR 1; 6.
DR PRINTS; PRO0019; LEURICHRT.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00013; LRRNT; 1.
DR SMART; SM00365; LRR SD22; 4.
DR SMART; SM00369; LRR_Typ; 8.
DR PROSITE; PS00022; EGF 1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00026; EGF 3; 1.
DR PROSITE; PS00853; FN3; 1.
SQ SEQUENCE 673 AA; 71712 MW; 891E149652DEA286 CRC64;

Query Match 98.2%; Score 3078.5; DB 2; Length 673;
Best Local Similarity 88.6%; Pred. No. 28-165; 2; Indels 75; Gaps 1;
Matches 596; Conservative 0; Mismatches 0;

Qy 1 MCSRVPVLLPLLLALLGPGVQCGSCGQCOPQTVFCTAROGTTVPRDVPDVTGLYVF 60
Db 1 MCSRVPVLLPLLLALLGPGVQCGSCGQCOPQTVFCTAROGTTVPRDVPDVTGLYVF 60
Qy 61 ENGITWLDASSPAGLPGQLDLSQNIAS----- 90
Db 61 ENGITWLDAGSPAGLPGQLDLSQNIASLPSGVFQPLANLSNLDLTANRLHEITNFT 120
Qy 91 ----- 105
Db 121 RGLRLRLRYLGNKRIHQPGAFDRLDLRLLEKLQDNELRALPRLRLDLLDLSHNS 180
Qy 106 LLALRPGILDTANVEALRIAGLGLQQLDEGLFRLRLNHLHDLDVSDNQLRVPVIRGLRG 165
Db 181 LLALRPGILDTANVEALRIAGLGLQQLDEGLFRLRLNHLHDLDVSDNQLRVPVIRGLRG 240
Qy 166 LTRLRAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLGLFPRRLILAAARNPF 225
Db 241 LTRLRAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLGLFPRRLILAAARNPF 300
Qy 226 NCVCPLSWFGPWVRESHVTLASPEETRCHFPKPNAGRLLELDYADFGCPATTTATVPT 285
Db 301 NCVCPLSWFGPWVRESHVTLASPEETRCHFPKPNAGRLLELDYADFGCPATTTATVPT 360
Qy 286 TRPVREPTALSSSLAPTWSPTAPATEAPSPSTAPPTVGPVPOQDCPPSTCLNGGTC 345
Db 361 TRPVREPTALSSSLAPTWSPTAPATEAPSPSTAPPTVGPVPOQDCPPSTCLNGGTC 420
Qy 346 HLGTRHHLACLCEGFTGLYCESQMGQTRPSPTVTPRPSRLTLGIEPVSPSLRVGL 405
Db 421 HLGTRHHLACLCEGFTGLYCESQMGQTRPSPTVTPRPSRLTLGIEPVSPSLRVGL 480
Qy 406 QRYLOGSSVOLRLTYRNLSGPDKRLVTLRLPASLAETVTLQRPNATYSVCVMPGLP 465
Db 481 QRYLOGSSVOLRLTYRNLSGPDKRLVTLRLPASLAETVTLQRPNATYSVCVMPGLP 540
Qy 466 GRVPEGEACGEAHTPPAVHNSHAPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVR 525
Db 541 GRVPEGEACGEAHTPPAVHNSHAPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVR 600
Qy 526 RGRMAAAAQDKGVQFGAGPLEGKVKVPLEPGPKATGGGEALPSGSECEVPLMGFPF 585
Db 601 RGRMAAAAQDKGVQFGAGPLEGKVKVPLEPGPKATGGGEALPSGSECEVPLMGFPF 660
Qy 586 PGLQSPHLHAKPYI 598
Db 661 PGLQSPHLHAKPYI 673

RESULT 4
Q96CX1 HUMAN
ID Q96CX1 HUMAN PRELIMINARY; PRT; 601 AA.
AC Q96CX1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)


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DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE SLIT12 protein (Fragment).
GN Name=Slit12;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388251; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smal M.A.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RG NIH MGC Project;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013767; AAH13767.1; -; mRNA.
DR HSSP; Q9BZ66; 1P8T.
DR Ensembl; ENSG00000168140; Homo sapiens.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR Cterm.
DR InterPro; IPR003591; LRR_Typ.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF01463; LRRT; 1.
DR Pfam; PF00560; LRR 1; 6.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00060; FN3; 1.
DR SMART; SM00082; LRRT; 1.
DR SMART; SM00369; LRR_Typ; 2.
DR PROSITE; PS00022; EGF 1; 1.
DR PROSITE; PS01186; EGF 2; 1.
DR PROSITE; PS00026; EGF 3; 1.
DR PROSITE; PS00853; FN3; 1.
KW EGF-like domain; Leucine-rich repeat.
FT NON_TER 1
SQ SEQUENCE 601 AA; 64178 MW; 496407F778D9ABD2 CRC64;

Query Match 86.0%; Score 2697.5; DB 2; Length 601;
Best Local Similarity 87.4%; Pred. No. 5.4e-144;
Matches 525; Conservative 0; Mismatches 1; Indels 75; Gaps 1;

QY 73 AGLPGLQLDLDSQNIQAS-----
DB 1 AGLPGLQLDLDSQNIQASLPGVQFPLANLSNLDLTANRLHETITNFTFGLRLRLRYLG 60

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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Giassi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Kingwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugihara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Tanigawa S., Tanaka Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK083684; BAC38992.1; -; mRNA.
DR HSSP; P00740; 1EDM.
DR MGI; MGI:2177651; Slit12.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR006210; IEFG.
DR InterPro; IPR001611; LRR.

DR InterPro; IPR000483; LRR Cterm.
DR InterPro; IPR000372; LRR Nterm.
DR InterPro; IPR003591; LRR_typ.
DR Pfam; PF00008; EGF_1.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF01463; LRRCT; 1.
DR Pfam; PF01462; LRRNT; 1.
DR Pfam; PF00560; LRR 1; 6.
DR PRINTS; SM00019; LEURICHRPT.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00060; FN3; 1.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00013; LRRNT; 1.
DR SMART; SM00369; LRR_TYP; 3.
DR PROSITE; PS00022; EGF 1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS00853; FN3; 1.
KW Hypothetical protein; lipoprotein.
SQ SEQUENCE 673 AA; 72284 MW; E35D1B35DDFF5EDB CRC64;
Query Match 79.5%; Score 2491; DB 2; Length 673;
Best Local Similarity 73.5%; Pred. No. 2.6e-132;
Matches 491; Conservative 25; Mismatches 74; Indels 78; Gaps 3;
QY 6 PLLLP LLLLLLALGPGVQCPCGCGCQCPQVFCFCTARQGTTPRQVPPDTPVGLYVFENGIT 65
DB 9 PLL--LLLLLVLLGSGVQCPCGCGCQCPQVFCFCTARQGTTPRQVPPDTPVGLYVFENGIT 66
QY 66 MLDASSFAGLPGLQLLLDLSQNOIAS-----LRLPRLLLLDLSHNSLLALE 110
DB 67 TLDVGCFAGLPGLQLLLDLSQNOITS LPGGIFQPLVNLNLDLTANKLHEISNETPRGLRR 126
QY 91 -----LRLPRLLLLDLSHNSLLALE 110
DB 127 LERLYLGKNI RHIPQGFADLRLELKLPNELRVLPPLRLPLRLLLDLSHNSIPALE 186
QY 111 PGILDNTANVEALRLAGLQQLDEGLFSRLNHLNLDVSDNQLERVPVPIRGLGLTRLR 170
DB 187 AGILDNTANVEALRLAGLQQLDEGLFORLNLNHLNLDVSDNQLHEMPSVIQGLRGLTRLR 246
QY 171 LAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDSLGLFPRLRLAAARNPNCVCP 230
DB 247 LAGNTRIAQIRPEDLAGLALQELDVSNLSLQALPSDLSLFPRLRLAAARNPNCVCP 306
QY 231 LSWGPGWRESHVTLASPEETRCHFPKPNAGRLLELDYADGCGCATTTTATVTPRPV 290
DB 307 LSWFGPWRENVHVLASPEETRCHFPKPNAGRLLELDYADGCGCATTTTATVTPRSTI 366
QY 291 REPTALSSSLAPTWLSPTAPATEAPSPDPTAPTPVGPVQPDQCPSPCLNGGTCHLGR 350
DB 367 REPTLSTSSQAPTWSHTEPTQASTVLTSTAPTPWPAPOQDCPDASICLNGGSCRLGAR 426
QY 351 HHLACLCEPGTGLYCSEMQGQTRPSPTVTPRPSRLTGLIEPVSPTSRLVGLQRYLQ 410
DB 427 HHWECLCEPGTGLYCSEPVQGMKPSIPDTPRPPPLPLSIEPVSPTSRLVGLQRYLQ 486
QY 411 GSSVQLASRLTYRNLSPDKRLTLRLPASLAETVTLRPNATYSVCVWPLGGRVPE 470
DB 487 GNTVQLASRLTYRNLSPDKRLVTLRLPASLAETVTLRPNATYSVCVPLGAGRTP 546
QY 471 GEEACGEAHTPPVHSHNHPVQTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAM 530
DB 547 GEEACGEANTSQVRSNHPVQTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRARA- 605
QY 531 AAAAQDKGVGPGAGPLEGKVPLEPGPKATGEGGALPSGSECEVPLMGFGPGGQLQS 590
DB 606 TSAQDKGVGPGTGLEGKVPLEPGKATGEGGALPSGSECEVPLMGFGPGGQLQS 665
QY 591 PLHAKPYI 598
DB 666 VLPKHYI 673

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RESULT 6
Q8R2G5_MOUSE PRELIMINARY; PRT; 673 AA.
AC Q8R2G5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Slit-like 2 protein precursor.
GN Name=Slit2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Schrewe H., Kutejova E.;
RT "Structure and expression analysis of the mouse Slit-like 2 (Slit2)
RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
RA Stapleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Hellon E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Kidney;
RA Director MGC Project;
RL Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ458938; CAD30331.1; -; mRNA.
DR EMBL; BC050274; AAH50274.1; -; mRNA.
DR HSSP; P00740; 1EDM.
DR Ensembl; ENSMUSG00000039646; Mus musculus.
DR MGI; MGI:217651; Slit2.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR Cterm.
DR InterPro; IPR000372; LRR Nterm.
DR InterPro; IPR003591; LRR typ.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF01463; LRRCT; 1.
DR Pfam; PF01462; LRRNT; 1.
DR Pfam; PF00560; LRR 1; 6.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00060; FN3; 1.
DR SMART; SM00082; LRRCT; 1.
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DR SMART; SM00013; LRRNT; 1.
DR SMART; SM00369; LRR_TYP; 3.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS50026; EGF_3; 1.
DR PROSITE; PS50853; FN3; 1.
KW Signal.
FT SIGNAL. 1 24 Potential.
FT CHAIN 25 673 Slit-like 2 protein.
SQ SEQUENCE 673 AA; 72260 MW; AAB8DA82DA8B9D32 CRC64;

Query Match 79.4%; Score 2490; DB 2; Length 673;
Best Local Similarity 73.5%; Pred. No. 3e-132;
Matches 491; Conservative 25; Mismatches 74; Indels 78; Gaps 3;

QY 6 PLLLP LLL L L L L A L G P V G C G C P S G C C Q S Q P Q T V F C T A R Q G T T V P R D V P P D T V G L Y F E N G I T 65
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 9 PLL-- L L L L V L L G S V G C G C P S G C C Q N Q P Q T V F C T A R Q G T T V P R D V P P D T V G L Y F E N G I T 66

QY 66 M L D A S S F A G L F G L Q L L D L S Q N Q I A S ----- L R L P R L L L D L S H N S L L A L E 110
   ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db 67 T L D V G C F A G L F G L Q L L D L S Q N Q I T S L P G G I F Q P L V N L S N L D L T A N K L H E I S N E T F R G L R R 126

QY 91 ----- L R L P R L L L D L S H N S L L A L E 110
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Db 127 L E R L Y L G K N R I R H I Q P G A F D A L D R L L E L K L P D N E L R V L P P L H L P R L L L D L S H N S I P A L E 186

QY 111 P G I L D T A N V E A L R L A G L G L Q L D E G L F S R L R N L H D L D V S D N Q L E R V P P V I R G L R G L T R L R 170
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Db 187 A G I L D T A N V E A L R L A G L G L R Q L D E G L F G R L N L H D L D V S D N Q L E H M P S V I Q L R G L T R L R 246

QY 171 L A G N T R I A Q L P E D L A G L A L Q E L D V S N L S Q A L P G D L S G L F P P R L L L A A A R N P N C V C P 230
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Db 247 L A G N T R I A Q I P E D L A G L T A L Q E L D V S N L S Q A L P S D L S L F P P R L L L A A A R N P N C L C P 306

QY 231 L S W F G P W R E S H V T L A S P E E T R C H F P P K N A G R L L L E L D Y A D F G C P A T T T T A T V P T T R P V 290
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Db 307 L S W F G P W R E N H V L A S P E E T R C H F P P K N A G R L L L D L D Y A D F G C P V T T T T A T V P I R S T I 366

QY 291 R E P T A L S S L A P T W L S P T A P A T E A P S P S T A P P T V G V P V P Q D C P P S C L N G T C H L G T R 350
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Db 367 R E P T L S T S S Q A P T W P S L T E P T T Q A S T V L S T A P P T M R P A P Q P Q D C P A S I C L N G S C R L G A R 426

QY 351 H H L A C L C E G T G L Y C E S Q M Q C T R P S P T P T P P R S L T I G I E P V S T S L R V G L Q R Y L Q 410
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 427 H H W E C L C P E G I G L Y C E S P V E Q G M K P S S I P P T P R P P L L P L S I E P V S T S L R V K L Q R Y L Q 486

QY 411 G S S V Q L R S L R L T Y R N L S G P D K R L V T L R L P A S L A E Y T V T Q L R P N A T Y S V C V M P L G P G R V P E 470
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Db 487 G N T V Q L R S L R L T Y R N L S G P D K R L V T L R L P A S L A E Y T V T Q L R P N A T Y S I C V T P L G A G R T P E 546

QY 471 G E E A C G E A H T P P A V H S N H A P V T Q A R E G N L P L L I A P A L A A V L L A A L A A V G A A Y C V R R G R A M 530
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 547 G E E A C G E A N T S Q A V R S N H A P V T Q A R E G N L P L L I A P A L A A V L L A A A G A A Y C V R R A R A - 605

QY 531 A A A A Q D K G V G P G A G P L E G V K V P L E P G P K A T E G G E A L P S G S C E F V P L M G F P P G L O S 590
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 606 T S T A Q D K G V G P G T G P L E G V K A P L E P G S K A T E G G E A L S G G P E C E V P L M G Y P G P L Q G 665

QY 591 P L H A K P Y I 598
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Db 666 V L P A K H Y I 673

RESULT 7
Q8CZT5_MOUSE PRELIMINARY; PRT; 673 AA.
AC Q8CZT5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 10 days embryo whole body cDNA, RIKEN full-length
DE enriched library, clone:2610528G05 product:hypothetical Prokaryotic
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DE membrane lipoprotein lipid attachment site/Cysteine-rich flanking
 DE region, N-terminal/Leucine-rich repeat/EGF-like domain/Leucine-rich
 DE repeat, typical subtype/Leucine-rich repeat, outliers/Cysteine-rich
 DE flanking region, C-terminal/Leucine-rich region/Fibronectin type III
 DE domain containing protein, full insert sequence.
 GN Names-Slit12;
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RX MEDLINE=21085660; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.
 RT "High-efficiency full-length cDNA cloning."
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Glessi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Mateu Y., Nikaudo I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Maehina J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RA The PANTOM Consortium.
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes."
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kusunagi T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohata E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer."
 RL Genome Res. 10:1757-1771(2000).

RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
 RA Matsumoto T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Sakai K.,
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Shiraki T.,
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK012169; BAB28075.1; -; mRNA.
 DR HSSP; P00740; 1EDM.
 DR Ensembl; ENSMUSG00000039646; Mus musculus.
 DR MGI; MGI:2177851; Slit12.
 DR InterPro; IPR000742; EGF 2.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR003961; FN III.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000483; LRR Cterm.
 DR InterPro; IPR000372; LRR Nterm.
 DR InterPro; IPR003591; LRR typ.
 DR Pfam; PF00008; EGF 1.
 DR Pfam; PF00041; fn3; 1.
 DR Pfam; PF01463; LRRCT; 1.
 DR Pfam; PF01462; LRRNT; 1.
 DR Pfam; PF00560; LRR 1; 6.
 DR PRINTS; PR00019; LEURICHRPT.
 DR SMART; SM00181; EGF 1.
 DR SMART; SM00060; FN3; 1.
 DR SMART; SM00082; LRRCT; 1.
 DR SMART; SM00013; LRRNT; 1.
 DR SMART; SM00369; LRR typ; 3.
 DR PROSITE; PS00022; EGF 1; UNKNOWN_1.
 DR PROSITE; PS01186; EGF 2; 1.
 DR PROSITE; PS50026; EGF_3; 1.
 DR PROSITE; PS50853; FN3; 1.
 DR Hypothetical protein; lipoprotein.
 SQ SEQUENCE 673 AA; 72336 MW; 9C53F90ADF43PBD9 CRC64;
 Query Match 79.2%; Score 2484; DB 2; Length 673;
 Best Local Similarity 73.4%; Pred. No. 6.6e-132;
 Matches 490; Conservative 25; Mismatches 75; Indels 78; Gaps 3;
 QY 6 PLLLP LLLLLLALPGVQCGPCGCGCQCPQTVFCTARQGTTPRDPVPPDTVGLYVPENGIT 65
 DB 9 PLL-- LLLLLLGSVQCGPCGCGCQCPQTVFCTARQGTTPRDPVPPDTVGLYVPENGIT 66
 QY 66 MLDASSFAGLPGLQLDLDSQNIAS-----LRLPLLILDLSHNSLLALE 110
 DB 67 TLDVGCFAGLPGLQLDLDSQNIATSLPGGIFQPLVNLNLDLTANKLHEISNETRGLRR 126
 QY 91 -----LRLPLLILDLSHNSLLALE 110
 DB 127 LERLYLGNRIHIOPGAFDALDRLELKLDPNEURVLPPLHPLRLLDLLSHNSIPALE 186
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 QY 171 LAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDSLGLFPRLRLAAARNPNCVCP 230
 DB 247 LAGNTRIAQIRPEDLAGLTALQELDVSNLSLQALPSDLSSLPFRRLRLAAARNPNCVCP 306
 QY 231 LSWFGPWVREHVTLASPEETRCHPPKPNAGLLELDYADGCPATTTTATVTPTRPV 290
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QY 351 HHLACLCEGFTGLYCESOMGQGTSPPTVTPRPRSLTLGLIEPVSPSTSLRVGLQRYLQ 410
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QY 411 GSSVQLRSRLTYRNLSPDKRLVTLRLPASLAETVTVQLRNATYSCVWMLPGSRVPE 470
Db 487 GNTVQLRSRLTYRNLSPDKRLVTLRLPASLAETVTVQLRNATYSCVWMLPGAGRTPE 546
QY 471 GREACGEAHTPPAVHSHNAPVTVQAREGNLPLIIAPALAAVLLAAAGAAVCVRGRAM 530
Db 547 GEAACGEANTSQAVSHNAPVTVQAREGNLPLIIAPALAAVLLAAAGAAVCVRGRAM - 605
QY 531 AAAADKQGVGAGGLEGVKVPLEPGPKATEGGGALPGSGSCEVPLMGFPFGPLQS 590
Db 606 TSTAQDKGVGPGTGLEGVKAPLEPGPKATEGGGALPGSGSCEVPLMGYPGSLQG 665
QY 591 PLHAKPYI 598
Db 666 VLPKHYI 673

RESULT 9

ID Q6DF55_XENTR PRELIMINARY; PRT; 661 AA.
AC Q6DF55;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE MGC88956 protein.
GN Name=MGC88956;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus; Silurana.
OX NCBI_TaxId=8364;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]

NUCLEOTIDE SEQUENCE.

RP TISSUE=whole body;
RC Klein S., Gerhard D.S.;
RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC076888; AAH76888.1; -; mRNA.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001611; LRR.

DR InterPro; IPR000483; LRR Cterm.
DR InterPro; IPR003885; LRR_cyst.
DR InterPro; IPR003591; LRR_typ.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF01463; LRRCT; 1.
DR Pfam; PF00560; LRR; 1; 8.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00365; LRR_SD22; 4.
DR SMART; SM00369; LRR_TYP; 6.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00026; EGF_3; 1.
SQ SEQUENCE 661 AA; 71957 MW; A0AC479468B8DBEA CRC64;

Query Match 38.7%; Score 1213.5; DB 2; Length 661;
Best Local Similarity 41.3%; Pred. No. 2.6e-60;
Matches 282; Conservative 88; Mismatches 158; Indels 155; Gaps 20;

QY 8 LIPLLLLLALGPGV--QCPSGCCSQDQTVFCARQGTTPRDPVPPVTVGLYVPENGIT 65
Db 4 LLVMIILLATAQOMITEGCPAGCQCNTPQTVFCARKNSNFPSPVPPDTLLNLYVFENGIS 63
QY 66 MLDASSFAGLPGLQLLDLSQNIASL----- 91
Db 64 SISSSFGLNGLHLLDLSHNLQSLPGCVFRNLANLNLDTSNLQTEISADTFQGLSR 123
QY 92 -----RLPRLLLLDLSHNSLLALE 110
Db 124 LERLYLNGNRIRSIHPEAFKGISSLKLNQNLVTPPAFSLPHLLLLDSYNAIPVQI 183
QY 111 PGILDANVEALRAGLGLQDLDEGLFSRLRNLDHLDVSDNQLERVPVPIGLRLGLTLRL 170
Db 184 QGVFNAGNIESRLRAGLGLKEVPBELLGSLKNLHDLSDNQDKVPP---GLHGLTKLN 240
QY 171 LAGNTRIAQLRPDLAGLAAQLDQVNSLSQALPGDLSGLFPRLRLAAARNPNCVCP 230
Db 241 IAGNVGFSQIQVDDLSNLPALQELDSLGLSLQTLFKGLFRSSKRLRAVSLAQNPNCVCS 300
QY 231 LSWFGPWVRESHVTLASPEETRCHFPKPNAGRLLELDYADFGCPATTTTATVTPTRPVV 290
Db 301 LGWLSEWNRVSGVLLRDETRCHFPKPNAGRLLELDYADFGCPATTTTATVTPTRPVV 358
QY 291 REPTALSSSLAPTWLSPTAP---ATEAPSPSTAPPTVGPVPOD-----CP 335
Db 359 -----STTTGP-----PTTKHLQTEAPTTASTTTTTIPHQEQEEDTQPFQDFEDTLCP 408
QY 336 PSTCLNGTCHLQTRHHLACLCPGFTGLYCESQMGQGTSPPTVTPRPRSL---TLG 392
Db 409 PQTCLNGSGCHLDPTGQLECCPPGFQGYCYET-----GPVTFAVTEMVIEQVK 458
QY 393 IEPVSPTSLRVGLQRYLQSSSVQLRSRLTYRNLSPGDKRLVTLRLPASLAETVTVQLRP 452
Db 459 IIEVTVSIRVDLQSYSNKE-KLRAIRLTVRNLYGADRRPMYKLPPTLPEYTVRALSS 517
QY 453 NATYSVCVMPILGPRVPEGEACCEAHT---PPAVHSHNAP-VTQAREGNLPLIIAPALA 508
Db 518 NSSYVWVLGSGQEGG-PE-EDLCTETHTLGEPF-----KHSQVTSQSGNLTLLVLPAPA 571
QY 509 AVLLAALAAVCAACVVRGRAMAAADKQGVGAGPLGKVLGKVPLEPGPKATEGGGE 568
Db 572 AGILLIS-AAVAAAACAYARR-----KKGSHSVEDGGPLEMDGVK-----KGLDGGKE 617
QY 569 AL-----PSGSECEVPLM 581
Db 618 VKLSESDPTGPEKTAESEEPML 640

RESULT 9

Q503G2 BRARE
ID Q503G2 BRARE PRELIMINARY; PRT; 643 AA.
AC Q503G2;

QY 292 EPTLSSSLAPTWLSPATAPAPSPSTAP-----PTVGPVPQOD----- 333
 Db 619 SETGTPSPVSTTTPPKMTYTNAIPTPPPPPEEILPSKTPPLPPEPTFSPSPSTGEVE 678
 QY 334 ---CPPTCLNGTCHLGRHHLACLCEGFTGLYCESQMGQTRPSPTVTPRPPR--- 387
 Db 679 SHICPANICLNGTCHFDPMGQLSCICLSGTSLGCEN-----VDIVDPKHPV 728
 QY 388 ---SLTLGIEP-----VSPTSRLVGLQRYLQGSVQLRSLRLLTYRNLSGPDKRLV 434
 Db 729 TEATLAASVPVQNDIAISRQVSTSIILDLQRFIE-TRPHIRGIRLLYRNLSGPDRRPM 787
 QY 435 TLRLPASLAEXTVTLRPNATYVSCVMPGLP-----GRVPEGEACEAHT----- 480
 Db 788 ILUSVPASPEYTLRGLKNCITYSCASPLGERVSRANSSVDTG--SCTEAKTEGILMTS 845
 QY 481 PPAVHSHNAPVTOAREGNLPLLIAPALAAVLLAALAAAGAAVCRVRGRAMAAADKQGV 540
 Db 846 SSATAPTCPMT-----FTLLIIVSALALVGLSVAGTVICVRK-RREKAGMELEWA 898
 QY 541 GPGAGPLEGKVKVPLEGPKKATGEGGALPSG-----SECEVPL 580
 Db 899 PADSDPMELDKMGLGANGT-----LPHKQAIINRCHTPL 936

RESULT 11

Q50LG9 HUMAN PRELIMINARY; PRT; 513 AA.
 AC Q50LG9;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE LRR24 protein.
 GN Name=LRR24;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RC TISSUE=Brain;
 RA Shimizu N., Asakawa S., Shimizu A., Yamazaki S., Ishikawa S.K.;
 RT "Novel gene containing Leucine rich repeat on human chromosome 8";
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB178281; BAD97811.1; -; mRNA.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig c2.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000483; LRR C-term.
 DR InterPro; IPR000372; LRR N-term.
 DR InterPro; IPR003591; LRR typ.
 DR Pfam; PF00560; LRR 1; 5_
 DR Pfam; PF01463; LRRCT; 1.
 DR PRINTS; PRO00019; LEURICHRPT.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00408; IGC2; 1.
 DR SMART; SM00369; LRR_TYP; 6.
 DR SMART; SM00082; LRRCT; 1.
 DR SMART; SM00013; LRRNT; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 KW Immunoglobulin domain; Leucine-rich repeat; Repeat.
 SQ SEQUENCE 513 AA; 55199 MW; 3770FA80D979C1DE CRC64;

Query Match 11.8%; Score 368.5; DB 2; Length 513;
 Best Local Similarity 26.4%; Pred. No. 8.5e-13;
 Matches 170; Conservative 63; Mismatches 217; Indels 195; Gaps 28;

QY 1 MCSRVPLLLPLLLALGFGVQSGCQSQPQTVFCTARQGTTPVPRDVPDVTGLYVF 60
 Db 1 MALRAPALLPLLLD-LPLRAAGCCPAACRC-YSATVEGALRLRVPLIGIPGTQTLFLQ 58

QY 61 ENGITMDASSFAGLPGIQLLDLSONQIASLRL-----PRLLLDLSHNSLLALEPG-I 113
 Db 59 DNNIARLEPGALAPLAALRRILYLNHNSLRALEAGAFRAQPRLELLELALTSNRLRGSRGAF 118
 QY 114 LDTANVEALRLAGLQQLDEGLFSRLRNLDLSDVSNQLERVPPVRLGRGLRLRLLAG 173
 Db 119 VGLAQLRVLYLAGNQLARLLDFTFLHPLRLQELHQLQENSIE----- 159
 QY 174 NTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRRLRLAAARNPNCVCLPSW 233
 Db 160 -----LLEDQALAGLSSLLALDLSRNQLTISREALQPLASLQVLRLTENPWRCDALHW 214
 QY 234 FGPVRESHVTLASPEETR--CHEPPKNAGRLLLLELDYADFGCPATTTTATVTPTRPVR 291
 Db 215 LGAMIKEGGKLLTSRDRKIMCABPFRLLALOSLLDVSLSLIC-----IPPSVHV-- 264
 QY 292 EPTLSSSLAPTWLSPATAPAPSPSTAPPTVGPVPQODCPP--STCLNGGTCILGT 349
 Db 265 QPLELTANLGED-LRVACQASGYQP-----LVTRKVPQPREGRPRAQAQLEGGL--LGL 317
 QY 350 RHHLACLCEGF-----TGLY-CESQMGQ-----TRPSP-TPVTPRP 385
 Db 318 GGHASDTGSGMLFLSNITLAHAGKYCEASNAGGAARVFRLLVNASRQQPQQAQPPP 377
 QY 386 PRSLTLGIEPVSPTSLRVGLQRYLQGSVQLRSLRLLTYRNLSGPDKRLVLRPLASLA 445
 Db 378 PAARPAGSEP----- 387
 QY 446 TVTQLRPNATYVSCVMPGLGPRVPEGEACGEAHTPPAVHSHNAPVTQAREGNLPLLIAP 505
 Db 388 -----RPEAG-SMAFRALG-----VATQT-----ATAA 409
 QY 506 ALAAVLLAALAAVGAAYCVRRGRAMAAADKQVPGCA-----GP-----LELEGVK- 553
 Db 410 AIALIALTALLV-AMICRRRRRKKK-----RGPPEGALFVNDYLDGPTCTFAQLEELRD 464
 QY 554 -----VPLEPFGPKATGEGGALPSGSECEVPLMGFPFGGLQSP 591
 Db 465 ERGHEMFVNRKPLFAEGPAEA---PADCG-PAQG-AGPGLRVP 504

RESULT 12

LRFN4 HUMAN
 ID LRFN4_HUMAN STANDARD; PRT; 635 AA.
 AC Q6PUG9; Q9BWJ0;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Leucine-rich repeat and fibronectin type-III domain containing protein
 DE 4 precursor.
 GN Name=LRFN4;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RC NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RP TISSUE=Eye, and Lung;
 RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Saeki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.

"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs"; Nature 420:563-573 (2002).

[2]

NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

STRAN=FBV/N; TISSUE=Eye, and Mammary tumor;

MDLLINE=22388257; PubMed12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L., Scapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udén T.B., Tothiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).

CC -1- SIMILARITY: Contains 1 fibronectin type-III domain.

CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.

CC -1- SIMILARITY: Contains 7 LRR (leucine-rich) repeats.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

DR ENBL; AK081560; BAC38259.1; -; mRNA.

DR ENBL; BC023036; AAH23036.1; -; mRNA.

DR ENBL; BC023156; AAH23156.1; -; mRNA.

DR HSSP; Q9BZR6; 1P8T.

DR Ensembl; ENSMUSG0000045045; Mus musculus.

DR MGI; MGI:2385612; Lrfn4.

DR InterPro; IPR003961; FN_III.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR001611; LRR.

DR InterPro; IPR003591; LRR_type.

DR Pfam; PF00041; fn3; 1.

DR Pfam; PF00560; LRR_1; 6.

DR PRINTS; PR00019; LEURCHRP.

DR PROSITE; PSS0853; FN3; 1.

DR PROSITE; PSS0835; IG_Like; 1.

KW Glycoprotein; Immunoglobulin domain; Leucine-rich repeat; Repeat;

KW Signal; Transmembrane.

FT SIGNAL 1 16 Potential.

FT CHAIN 17 636 Leucine-rich repeat and fibronectin type-III domain containing protein 4.

FT TOPO_DOM 17 518 Extracellular (Potential).

FT TRANSMEM 519 539 Potential.

DT 01-MAR-2003 (TEMBLrel. 23, Created)
 DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
 DT 13-SEP-2005 (TEMBLrel. 31, Last annotation update)
 DE Mus musculus adult male aorta and vein cDNA, RIKEN full-length
 DE enriched library, clone:A530098L04 product:KIAA0405 (LEUCINE-RICH
 DE REPEAT TRANSMEMBRANE PROTEIN FLRT2) homolog (Fibronectin leucine rich
 DE transmembrane protein 2)
 GN Name=Map4k5; Synonym=1272;
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10099;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleschmann W., Gaasterland T., Glessi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guscinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Willing L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai J., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RA The FANTOM Consortium,
 RA "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format

RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akashira S., Tanaka T., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6xCBA;
 RA Haines B.P., Summerbell D., Rigby P.W.J.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N;
 RT TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
 RC virgin mouse. Taken by biopsy.
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.B., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustun T.B., Roshdyuk S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Bosak S.A., McEwan P.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [9]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N;
 RT TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
 RC virgin mouse. Taken by biopsy.
 RG NIH MGC Project;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK041311; BAC30900.1; -; mRNA.
 DR EMBL; AV495669; AAR92202.1; -; mRNA.
 DR EMBL; BC096471; AAN96471.1; -; mRNA.
 DR HSSP; P07359; IM0Z.
 DR Ensembl; ENSMUSG00000047414; Mus musculus.
 DR MGI; MGI:1925503; Map4k5.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR InterPro; IPR003961; FN III.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000483; LRR Cterm.
 DR InterPro; IPR000372; LRR Nterm.
 DR InterPro; IPR003591; LRR typ.
 DR InterPro; IPR001211; PhospholipaseA2.
 DR Pfam; PF00041; fn3; 1.
 DR Pfam; PF00560; LRR1; 8.
 DR Pfam; PF01463; LRRCT; 1.
 DR Pfam; PF01462; LRRNT; 1.
 DR PRINTS; PR00019; LEURICHRPT.

RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RN Genome Res. 10:1617-1630(2000).
 RL [5]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Olfactory brain;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kiseunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto K., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa K., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RA "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayaehida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kato H., Kawai J., Kojima T., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RL [7]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayaehida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kato H., Kawai J., Kojima T., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RA Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AK048678; BAC33419.1; -; mRNA.
 DR EMBL; AK078176; BAC37163.1; -; mRNA.
 DR HSP; Q98286; LOZN.
 DR Ensembl; ENSMUSG00000033707; Mus musculus.
 DR MGI; MGI:2445060; Lrrc14.
 DR GO; GO:0004180; F:carboxypeptidase activity; IEA.
 DR GO; GO:0008237; F:metallopeptidase activity; IEA.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_c2.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000483; LRR_Cterm.
 DR InterPro; IPR000372; LRR_Nterm.
 DR InterPro; IPR003591; LRR_Typ.
 DR Pfam; PF00560; LRR_1; 4.
 DR PRINTS; PR00019; LEURICHRPT.
 DR SMART; SM00408; IGC2; 1.
 DR SMART; SM00369; LRR_Typ; 3.
 DR SMART; SM00082; LRRCT; 1.
 DR SMART; SM00013; LRRNT; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Carboxypeptidase; Hypothetical protein; Immunoglobulin domain;
 KW Leucine-rich repeat; Metalloprotease; Protease; Repeat.
 SQ SEQUENCE 521 AA; 56334 MW; 3D1E4BEE302284A6 CRC64;

Query Match 10.8%; Score 339; DB 2; Length 521;
 Best Local Similarity 27.0%; Pred. No. 4e-11;
 Matches 149; Conservative 66; Mismatches 217; Indels 120; Gaps 21;
 QY 1 MCSRVPLLLPL---LLLLALGPGV-----QCGSGGCGCQSQPQTVCTARQTTVPRDVPDP 53
 DB 1 MALRAPTLLLLGLLLPLPPLPPLPRATGCPAARC-YSATVECCALRVVPPGIPPG 59
 QY 54 TVGLVVFENGITMLDASSFAGLPGQLLDLSNQIASLR-----LPRLLLDLSNSLL 107
 DB 60 TQTLFLQDINSIAHLEQSLAPLAARHLVHNNTLRALESAGFAFRAQPRLELALTGNRL 119
 QY 108 ALEPG-ILDTANVEALRLAGLGLQQLDEGLFRLRLNHLVDSDNQLERVPVIRGLRGL 166
 DB 120 GLRGAFVGLVQLRVLYLAGNLAKLLDFTFLHLPLQLHLQENSIE----- 167
 QY 167 TRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSQALPGDLSGLFPRLRLIAAARNPFN 226
 DB 168 -----LLEDQALAGLSLALLDLRSNQLGTISKALQPLSSQLVRLTENPWR 215
 QY 227 CVCPLSWFGPVRSHVTLASPEETR--CHFPPKNAGRLLLLELDYADFQCPATTTTATVP 284
 DB 216 CDCALHWLGSWIKEGRRLLSRDKKITCAEPRLALQSLLEVSGLSIC-----IP 267
 QY 285 TTRPVVREPTALSSSLAPTWSLPTAPATEAPSPPTAPPTVGVPOQDCPP--STCLNG 342
 DB 268 PSNVV--EPPEFTANLGED-LQVACQASGYPOP-----LVVWRKVQPRDGKPOAQALLEG 320
 QY 343 GTCHLG-----TRHHLACLCPGFTGLY-CESQMGQGTREPSPTFTVTPRPPR 387
 DB 321 GAPGLGHHGTRDTGSMPLFTNITLA-----HAGKYCEAAANAGGKARVPPHLLVNASR 374
 QY 388 SLTLGI-EPVSPSTSLRVGLQRLVQSSVQLRSRLRLTYRNLSPGDKRLVTL----- 436
 DB 375 QOSQQLPDPQAPATRPVGHPEQHEAGSMAFRALGLATQTATTAIALTALTALLAAMIC 434
 QY 437 -----RLPASLAEYV-----VTQLRPNATYSVCM-----PLGPGRVPE 470
 DB 435 RRRRRKKVPAPSGSGTLFVNDYSDGCTCTAQLBELRQDHGHEMFIDRSKPLFPPEVLP- 493
 QY 471 GEEACGEAHTPP 482
 DB 494 -EEA--PEHNPP 502
 Search completed: February 7, 2006, 16:17:42
 Job time : 283 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 7, 2006, 16:21:46 ; Search time 49 Seconds
(without alignments)

1008.981 Million cell updates/sec

Title: US-10-677-669-69

Perfect score: 3135

Sequence: 1 MCSRVLPLPLLLALLGPG.....PLMGFPGLQLHAKPYI 598

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Issued Patents AA:*

1: /cgn2_6/prodata/1/iaa/5 COMB.pep:*

2: /cgn2_6/prodata/1/iaa/6 COMB.pep:*

3: /cgn2_6/prodata/1/iaa/H COMB.pep:*

4: /cgn2_6/prodata/1/iaa/PCUTS COMB.pep:*

5: /cgn2_6/prodata/1/iaa/RE COMB.pep:*

6: /cgn2_6/prodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3135	100.0	598	2	US-09-866-028-69 Sequence 69, Appl
2	3135	100.0	598	2	US-09-944-457-69 Sequence 69, Appl
3	3135	100.0	598	2	US-09-945-584-69 Sequence 69, Appl
4	3135	100.0	598	2	US-09-944-944-69 Sequence 69, Appl
5	3135	100.0	598	2	US-09-945-587-69 Sequence 69, Appl
6	1083.5	98.4	673	2	US-09-063-950-2 Sequence 2, Appl
7	1083.5	98.4	673	2	US-09-991-181-52 Sequence 52, Appl
8	1083.5	98.4	673	2	US-09-990-444-52 Sequence 52, Appl
9	1083.5	98.4	673	2	US-09-997-333-52 Sequence 52, Appl
10	1083.5	98.4	673	2	US-09-992-598-52 Sequence 52, Appl
11	337	10.7	653	2	US-09-520-781-10 Sequence 10, Appl
12	337	10.7	653	2	US-09-957-187-10 Sequence 10, Appl
13	337	10.7	653	2	US-09-991-053-10 Sequence 10, Appl
14	333	10.6	590	2	US-09-520-781-12 Sequence 12, Appl
15	333	10.6	590	2	US-09-957-187-12 Sequence 12, Appl
16	333	10.6	590	2	US-09-991-053-12 Sequence 12, Appl
17	330	10.5	653	2	US-09-991-053-12 Sequence 12, Appl
18	330	10.5	653	2	US-09-990-444-229 Sequence 229, Appl
19	330	10.5	653	2	US-09-997-333-229 Sequence 229, Appl
20	330	10.5	653	2	US-09-992-598-229 Sequence 229, Appl
21	322	10.3	605	2	US-09-063-950-5 Sequence 5, Appl
22	320	10.2	660	2	US-09-907-794A-28 Sequence 28, Appl
23	320	10.2	660	2	US-09-905-125A-28 Sequence 28, Appl
24	320	10.2	660	2	US-09-902-775A-28 Sequence 28, Appl
25	320	10.2	660	2	US-09-906-700-28 Sequence 28, Appl
26	320	10.2	660	2	US-09-903-603A-28 Sequence 28, Appl
27	320	10.2	660	2	US-09-904-920A-28 Sequence 28, Appl

660	2	US-09-949-016-6843	10.2	320	28	Sequence 6843, Ap
660	2	US-09-909-064-28	10.2	320	29	Sequence 28, Appl
660	2	US-09-905-381A-28	10.2	320	30	Sequence 28, Appl
660	2	US-09-906-618-28	10.2	320	31	Sequence 28, Appl
660	2	US-09-906-646-28	10.2	320	32	Sequence 28, Appl
660	2	US-09-689-486-58	10.2	320	33	Sequence 58, Appl
660	2	US-09-904-462-28	10.2	320	34	Sequence 28, Appl
660	2	US-09-902-736A-28	10.2	320	35	Sequence 28, Appl
660	2	US-09-906-722A-28	10.2	320	36	Sequence 28, Appl
683	2	US-09-949-016-7267	10.2	320	37	Sequence 7267, Ap
674	2	US-09-689-486-59	9.9	310.5	38	Sequence 59, Appl
674	2	US-09-689-486-60	9.9	310.5	39	Sequence 60, Appl
662	2	US-09-949-016-10298	9.9	310	40	Sequence 10298, A
649	2	US-09-689-486-57	9.8	308	41	Sequence 57, Appl
674	2	US-09-949-016-7204	9.8	307.5	42	Sequence 7204, Ap
674	2	US-09-689-486-7	9.8	307.5	43	Sequence 7, Appl
605	1	US-08-190-802A-49	9.6	302	44	Sequence 49, Appl
605	2	US-08-477-346-49	9.6	302	45	Sequence 49, Appl
605	2	US-08-473-089-49	9.6	302	46	Sequence 49, Appl
605	2	US-08-487-072A-49	9.6	302	47	Sequence 49, Appl
605	2	US-09-538-092-1087	9.6	302	48	Sequence 1087, Ap
623	2	US-09-949-016-10995	9.6	302	49	Sequence 10995, A
448	2	US-09-520-781-32	9.6	301	50	Sequence 32, Appl
448	2	US-09-957-187-32	9.6	301	51	Sequence 32, Appl
448	2	US-09-991-053-32	9.6	301	52	Sequence 32, Appl
649	2	US-09-188-930-305	9.5	298.5	53	Sequence 305, App
649	2	US-09-312-283C-305	9.5	298.5	54	Sequence 305, App
640	2	US-09-907-794A-232	9.3	292.5	55	Sequence 232, App
640	2	US-09-905-125A-232	9.3	292.5	56	Sequence 232, App
640	2	US-09-902-775A-232	9.3	292.5	57	Sequence 232, App
640	2	US-09-906-700-292	9.3	292.5	58	Sequence 292, App
640	2	US-09-903-603A-292	9.3	292.5	59	Sequence 292, App
640	2	US-09-904-920A-232	9.3	292.5	60	Sequence 232, App
640	2	US-09-909-064-232	9.3	292.5	61	Sequence 232, App
640	2	US-09-905-381A-232	9.3	292.5	62	Sequence 232, App
640	2	US-09-906-618-232	9.3	292.5	63	Sequence 232, App
640	2	US-09-906-646-232	9.3	292.5	64	Sequence 232, App
640	2	US-09-904-462-232	9.3	292.5	65	Sequence 232, App
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640	2	US-09-990-444-501	9.3	292.5	68	Sequence 501, App
640	2	US-09-997-333-501	9.3	292.5	69	Sequence 501, App
640	2	US-09-992-598-501	9.3	292.5	70	Sequence 501, App
713	2	US-09-907-794A-245	9.2	287.5	71	Sequence 245, App
713	2	US-09-905-125A-245	9.2	287.5	72	Sequence 245, App
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713	2	US-09-906-700-245	9.2	287.5	74	Sequence 245, App
713	2	US-09-903-603A-245	9.2	287.5	75	Sequence 245, App
713	2	US-09-904-920A-245	9.2	287.5	76	Sequence 245, App
713	2	US-09-909-064-245	9.2	287.5	77	Sequence 245, App
713	2	US-09-905-381A-245	9.2	287.5	78	Sequence 245, App
713	2	US-09-906-618-245	9.2	287.5	79	Sequence 245, App
713	2	US-09-906-646-245	9.2	287.5	80	Sequence 245, App
713	2	US-09-906-646-245	9.2	287.5	81	Sequence 245, App
713	2	US-09-904-462-245	9.2	287.5	82	Sequence 245, App
713	2	US-09-902-736A-245	9.2	287.5	83	Sequence 245, App
713	2	US-09-906-722A-245	9.2	287.5	84	Sequence 245, App
745	2	US-10-104-047-2855	9.1	284.5	85	Sequence 2855, Ap
745	2	US-10-104-047-2860	9.0	282.5	86	Sequence 2860, Ap
603	1	US-08-190-802A-50	9.0	281.5	87	Sequence 50, Appl
603	2	US-08-477-346-50	9.0	281.5	88	Sequence 50, Appl
603	2	US-08-473-089-50	9.0	281.5	89	Sequence 50, Appl
603	2	US-08-487-072A-50	9.0	281.5	90	Sequence 50, Appl
353	2	US-08-986-485-6	8.7	271.5	91	Sequence 6, Appl
1504	2	US-10-037-417-98	8.6	271.5	92	Sequence 98, Appl
473	2	US-09-949-016-8448	8.6	271	93	Sequence 8448, Ap
473	2	US-09-999-833A-400	8.6	271	94	Sequence 400, App
473	2	US-10-020-445A-400	8.6	271	95	Sequence 400, App
610	1	US-07-821-717B-6	8.3	259	96	Sequence 6, Appl
610	1	US-08-119-262B-6	8.3	259	97	Sequence 6, Appl
610	1	US-08-135-929A-11	8.3	259	98	Sequence 11, Appl
610	1	US-08-234-265A-11	8.3	259	99	Sequence 11, Appl
1523	2	US-09-182-024A-2	8.2	258	100	Sequence 2, Appl

101	258	8.2	1523	2	US-10-012-231A-198	Sequence 198, Appl	174	211	6.7	513	2	US-10-015-393A-385	Sequence 385, App
102	258	8.2	1523	2	US-10-015-389A-198	Sequence 198, Appl	175	211	6.7	513	2	US-10-011-833A-385	Sequence 385, App
103	258	8.2	1523	2	US-10-006-768A-198	Sequence 198, Appl	176	211	6.7	513	2	US-10-006-041A-385	Sequence 385, App
104	258	8.2	1523	2	US-10-015-671A-198	Sequence 198, Appl	177	211	6.7	513	2	US-10-012-064A-385	Sequence 5, Appl
105	258	8.2	1523	2	US-10-015-393A-198	Sequence 198, Appl	178	210.5	6.7	4302	2	US-08-658-136-8	Sequence 8, Appl
106	258	8.2	1523	2	US-10-011-833A-198	Sequence 198, Appl	179	210.5	6.7	4302	2	US-09-053-469-8	Sequence 8, Appl
107	258	8.2	1523	2	US-10-006-041A-198	Sequence 198, Appl	180	210.5	6.7	4302	2	US-08-422-582-8	Sequence 8, Appl
108	258	8.2	1523	2	US-10-012-064A-198	Sequence 198, Appl	181	210.5	6.7	4302	2	US-09-052-262-8	Sequence 8, Appl
109	255.5	8.1	1480	2	US-09-191-647-7	Sequence 7, Appl	182	209	6.7	353	2	US-10-012-231A-397	Sequence 397, App
110	255.5	8.1	1480	2	US-09-540-245A-7	Sequence 7, Appl	183	209	6.7	353	2	US-10-015-389A-397	Sequence 397, App
111	255.5	8.1	1480	2	US-09-540-153-7	Sequence 7, Appl	184	209	6.7	353	2	US-10-006-768A-397	Sequence 397, App
112	255.5	8.1	1480	2	US-09-182-024A-5	Sequence 5, Appl	185	209	6.7	353	2	US-10-015-671A-397	Sequence 397, App
113	255.5	8.1	1480	2	US-10-289-776-7	Sequence 7, Appl	186	209	6.7	353	2	US-10-015-393A-397	Sequence 397, App
114	255.5	8.1	1480	4	PCT-US91-09055-2	Sequence 2, Appl	187	209	6.7	353	2	US-10-011-833A-397	Sequence 397, App
115	253	8.0	566	2	US-10-037-417-106	Sequence 106, Appl	188	209	6.7	353	2	US-10-006-041A-397	Sequence 397, App
116	252	8.0	566	2	US-09-775-803-12	Sequence 12, Appl	189	209	6.7	353	2	US-10-012-064A-397	Sequence 397, App
117	252	8.0	567	2	US-10-037-417-105	Sequence 105, Appl	190	209	6.7	1091	2	US-08-986-485-5	Sequence 5, Appl
118	251	8.0	622	2	US-10-188-495-48	Sequence 48, Appl	191	208.5	6.7	424	2	US-09-949-016-7950	Sequence 7950, Ap
119	249.5	8.0	789	2	US-09-831-848-2	Sequence 2, Appl	192	207.5	6.6	415	2	US-09-935-430-659	Sequence 659, App
120	248	7.9	481	2	US-09-853-753-2	Sequence 2, Appl	193	207.5	6.6	440	2	US-09-964-956-29	Sequence 29, Appl
121	248	7.9	485	2	US-09-949-016-8704	Sequence 8704, Ap	194	207.5	6.6	798	2	US-09-935-430-658	Sequence 658, App
122	247.5	7.9	1525	2	US-09-191-647-2	Sequence 2, Appl	195	207.5	6.6	798	2	US-09-964-956-28	Sequence 28, Appl
123	247.5	7.9	1525	2	US-09-540-245A-2	Sequence 2, Appl	196	206.5	6.6	1101	2	US-08-986-485-2	Sequence 2, Appl
124	247.5	7.9	1525	2	US-09-540-153-2	Sequence 2, Appl	197	206	6.6	428	2	US-09-949-016-6625	Sequence 6625, Ap
125	247.5	7.9	1525	2	US-10-289-776-2	Sequence 2, Appl	198	206	6.6	433	2	US-09-949-016-8521	Sequence 8521, Ap
126	247.5	7.9	1529	2	US-10-188-495-67	Sequence 67, Appl	199	205	6.5	4339	2	US-09-052-469-6	Sequence 6, Appl
127	246.5	7.9	1529	2	US-09-312-283C-396	Sequence 396, App	200	205	6.5	4339	2	US-08-422-582-6	Sequence 6, Appl
128	244	7.8	708	2	US-09-131-648-2	Sequence 2, Appl	201	205	6.5	4339	2	US-09-052-262-6	Sequence 2, Appl
129	244	7.8	708	2	US-09-907-794A-69	Sequence 69, Appl	202	203.5	6.5	4303	1	US-08-460-751-2	Sequence 2, Appl
130	244	7.8	708	2	US-09-905-125A-69	Sequence 69, Appl	203	203.5	6.5	4303	2	US-09-479-467A-2	Sequence 2, Appl
131	244	7.8	708	2	US-09-902-775A-69	Sequence 69, Appl	204	203.5	6.5	4303	2	US-09-655-160-2	Sequence 2, Appl
132	244	7.8	708	2	US-09-906-700-69	Sequence 69, Appl	205	200.5	6.4	302	2	US-09-482-273-105	Sequence 105, App
133	244	7.8	708	2	US-09-903-603A-69	Sequence 69, Appl	206	200.5	6.4	724	2	US-10-104-047-2224	Sequence 2224, App
134	244	7.8	708	2	US-09-904-920A-69	Sequence 69, Appl	207	199	6.3	321	2	US-10-104-047-2504	Sequence 2504, Ap
135	244	7.8	708	2	US-09-909-064-69	Sequence 69, Appl	208	198.5	6.3	1338	2	US-09-631-603-2	Sequence 2, Appl
136	244	7.8	708	2	US-09-905-381A-69	Sequence 69, Appl	209	197.5	6.3	616	2	US-10-012-311A-24	Sequence 24, Appl
137	244	7.8	708	2	US-09-906-618-69	Sequence 69, Appl	210	197.5	6.3	616	2	US-10-015-389A-24	Sequence 24, Appl
138	244	7.8	708	2	US-09-906-646-69	Sequence 69, Appl	211	197.5	6.3	616	2	US-10-006-768A-24	Sequence 24, Appl
139	244	7.8	708	2	US-09-904-462-69	Sequence 69, Appl	212	197.5	6.3	616	2	US-10-015-671A-24	Sequence 24, Appl
140	244	7.8	708	2	US-09-902-736A-69	Sequence 69, Appl	213	197.5	6.3	616	2	US-10-015-393A-24	Sequence 24, Appl
141	244	7.8	708	2	US-09-906-722A-69	Sequence 69, Appl	214	197.5	6.3	616	2	US-10-011-833A-24	Sequence 24, Appl
142	243.5	7.8	312	2	US-10-037-417-108	Sequence 108, Appl	215	197.5	6.3	616	2	US-10-006-041A-24	Sequence 24, Appl
143	241	7.7	380	2	US-09-461-325-161	Sequence 161, App	216	197.5	6.3	616	2	US-10-012-064A-24	Sequence 24, Appl
144	241	7.7	380	2	US-10-012-542-161	Sequence 161, App	217	196.5	6.3	716	2	US-09-312-283C-183	Sequence 183, App
145	241	7.7	380	2	US-10-115-123-161	Sequence 161, App	218	196.5	6.3	771	2	US-09-188-930-183	Sequence 183, App
146	240	7.7	560	2	US-08-592-500-2	Sequence 2, Appl	219	195.5	6.2	553	2	US-10-037-417-28	Sequence 28, Appl
147	240	7.7	560	2	US-08-195-006-2	Sequence 2, Appl	220	195	6.2	620	2	US-09-907-794A-73	Sequence 73, Appl
148	240	7.7	560	2	US-09-063-950-4	Sequence 4, Appl	221	195	6.2	620	2	US-09-905-125A-73	Sequence 73, Appl
149	240	7.7	560	2	US-09-775-803-14	Sequence 14, Appl	222	195	6.2	620	2	US-09-902-775A-73	Sequence 73, Appl
150	240	7.7	560	4	PCT-US94-07644A-2	Sequence 2, Appl	223	195	6.2	620	2	US-09-906-700-73	Sequence 73, Appl
151	236.5	7.5	221	4	PCT-US91-09055-3	Sequence 3, Appl	224	195	6.2	620	2	US-09-903-603A-73	Sequence 73, Appl
152	236.5	7.5	221	4	US-08-986-485-7	Sequence 7, Appl	225	195	6.2	620	2	US-09-904-920A-73	Sequence 73, Appl
153	227	7.2	568	2	US-09-673-245-14	Sequence 14, Appl	226	195	6.2	620	2	US-09-909-064-73	Sequence 73, Appl
154	226.5	7.2	557	2	US-10-037-417-95	Sequence 95, Appl	227	195	6.2	620	2	US-09-905-381A-73	Sequence 73, Appl
155	225	7.2	735	2	US-09-191-647-9	Sequence 9, Appl	228	195	6.2	620	2	US-09-906-618-73	Sequence 73, Appl
156	225	7.2	735	2	US-09-540-245A-9	Sequence 9, Appl	229	195	6.2	620	2	US-09-906-646-73	Sequence 73, Appl
157	225	7.2	735	2	US-09-540-153-9	Sequence 9, Appl	230	195	6.2	620	2	US-09-904-462-73	Sequence 73, Appl
158	225	7.2	735	2	US-10-289-776-9	Sequence 9, Appl	231	195	6.2	620	2	US-09-902-736A-73	Sequence 73, Appl
159	222.5	7.1	536	2	US-09-538-092-992	Sequence 992, App	232	195	6.2	620	2	US-09-906-722A-73	Sequence 73, Appl
160	222	7.1	498	4	PCT-US91-09055-5	Sequence 5, Appl	233	195	6.2	742	2	US-10-104-047-2807	Sequence 2807, Ap
161	222	7.1	591	2	US-10-188-495-51	Sequence 51, Appl	234	195	6.2	832	2	US-09-935-430-660	Sequence 660, App
162	222	7.1	591	2	US-10-188-495-50	Sequence 50, Appl	235	195	6.2	853	2	US-09-964-956-30	Sequence 30, Appl
163	221.5	7.1	557	2	US-10-037-417-94	Sequence 94, Appl	236	194.5	6.2	699	2	US-09-949-016-6073	Sequence 6073, Ap
164	220.5	7.0	841	2	US-09-935-430-657	Sequence 657, App	237	194.5	6.2	720	2	US-09-949-016-9819	Sequence 9819, Ap
165	220.5	7.0	841	2	US-09-964-956-2	Sequence 2, Appl	238	193.5	6.2	224	4	PCT-US91-09055-4	Sequence 4, Appl
166	218.5	7.0	359	2	US-09-949-016-9732	Sequence 9732, Ap	239	193.5	6.2	542	2	US-10-037-417-97	Sequence 97, Appl
167	217.5	6.9	562	2	US-09-673-245-7	Sequence 7, Appl	240	190	6.1	1059	2	US-09-907-794A-290	Sequence 290, App
168	217.5	6.9	837	2	US-09-964-956-5	Sequence 52, Appl	241	190	6.1	1059	2	US-09-905-125A-290	Sequence 290, App
169	214.5	6.8	255	2	US-09-893-737-232	Sequence 232, Appl	242	190	6.1	1059	2	US-09-902-775A-290	Sequence 290, App
170	211	6.7	513	2	US-10-012-231A-385	Sequence 385, App	243	190	6.1	1059	2	US-09-906-700-290	Sequence 290, App
171	211	6.7	513	2	US-10-015-389A-385	Sequence 385, App	244	190	6.1	1059	2	US-09-903-603A-290	Sequence 290, App
172	211	6.7	513	2	US-10-006-768A-385	Sequence 385, App	245	190	6.1	1059	2	US-09-904-920A-290	Sequence 290, App
173	211	6.7	513	2	US-10-015-671A-385	Sequence 385, App	246	190	6.1	1059	2	US-09-909-064-290	Sequence 290, App

247	190	6.1	1059	2	US-09-905-381A-280	Sequence 290, App	320	167	5.3	746	4	PCT-US95-10509-2	Sequence 2, Appli
248	190	6.1	1059	2	US-09-906-618-290	Sequence 290, App	321	167	5.3	1112	2	US-09-353-585-3	Sequence 3, Appli
249	190	6.1	1059	2	US-09-906-646-290	Sequence 290, App	322	166.5	5.3	224	2	US-09-482-273-174	Sequence 174, App
250	190	6.1	1059	2	US-09-904-462-290	Sequence 290, App	323	166	5.3	1112	2	US-09-353-585-2	Sequence 2, Appli
251	190	6.1	1059	2	US-09-902-736A-280	Sequence 290, App	324	164.5	5.2	501	2	US-09-907-794A-185	Sequence 185, App
252	190	6.1	1059	2	US-09-906-722A-280	Sequence 290, App	325	164.5	5.2	501	2	US-09-905-125A-185	Sequence 185, App
253	190	6.1	1119	2	US-09-907-794A-280	Sequence 294, App	326	164.5	5.2	501	2	US-09-902-775A-185	Sequence 185, App
254	190	6.1	1119	2	US-09-905-125A-280	Sequence 294, App	327	164.5	5.2	501	2	US-09-906-700-185	Sequence 185, App
255	190	6.1	1119	2	US-09-902-775A-280	Sequence 294, App	328	164.5	5.2	501	2	US-09-903-603A-185	Sequence 185, App
256	190	6.1	1119	2	US-09-906-700-280	Sequence 294, App	329	164.5	5.2	501	2	US-09-904-920A-185	Sequence 185, App
257	190	6.1	1119	2	US-09-903-603A-280	Sequence 294, App	330	164.5	5.2	501	2	US-09-909-064-185	Sequence 185, App
258	190	6.1	1119	2	US-09-904-920A-280	Sequence 294, App	331	164.5	5.2	501	2	US-09-905-381A-185	Sequence 185, App
259	190	6.1	1119	2	US-09-909-064-280	Sequence 294, App	332	164.5	5.2	501	2	US-09-906-618-185	Sequence 185, App
260	190	6.1	1119	2	US-09-905-381A-280	Sequence 294, App	333	164.5	5.2	501	2	US-09-906-646-185	Sequence 185, App
261	190	6.1	1119	2	US-09-906-618-280	Sequence 294, App	334	164.5	5.2	501	2	US-09-904-462-185	Sequence 185, App
262	190	6.1	1119	2	US-09-906-646-280	Sequence 294, App	335	164.5	5.2	501	2	US-09-902-736A-185	Sequence 185, App
263	190	6.1	1119	2	US-09-904-462-280	Sequence 294, App	336	164.5	5.2	501	2	US-09-906-722A-185	Sequence 185, App
264	190	6.1	1119	2	US-09-902-736A-280	Sequence 294, App	337	164.5	5.2	501	2	US-09-908-149-8	Sequence 8, Appli
265	190	6.1	1119	2	US-09-906-722A-280	Sequence 294, App	338	164.5	5.2	582	2	US-09-908-149-8	Sequence 10752, A
266	186.5	5.9	196	4	PCT-US91-09055-6	Sequence 6, Appli	339	164.5	5.2	584	2	US-09-949-016-10752	Sequence 2918, Ap
267	186.5	5.9	844	2	US-09-949-016-9438	Sequence 9438, Ap	340	164	5.2	696	2	US-09-907-794A-91	Sequence 91, Appl
268	186	5.9	440	2	US-09-538-092-999	Sequence 999, App	341	164	5.2	696	2	US-09-905-125A-91	Sequence 91, Appl
269	186	5.9	451	2	US-09-949-016-9282	Sequence 9282, Ap	342	164	5.2	696	2	US-09-902-775A-91	Sequence 91, Appl
270	184	5.9	320	1	US-07-613-083B-1	Sequence 1, Appli	343	164	5.2	696	2	US-09-906-700-91	Sequence 91, Appl
271	184	5.9	368	2	US-09-949-016-6115	Sequence 6115, Ap	344	164	5.2	696	2	US-09-903-603A-91	Sequence 91, Appl
272	184	5.9	368	2	US-09-715-836A-9	Sequence 9, Appli	345	164	5.2	696	2	US-09-904-920A-91	Sequence 91, Appl
273	184	5.9	382	2	US-09-949-016-10542	Sequence 10542, A	346	164	5.2	696	2	US-09-909-064-91	Sequence 91, Appl
274	183	5.8	662	2	US-09-538-092-1325	Sequence 1325, Ap	347	164	5.2	696	2	US-09-905-381A-91	Sequence 91, Appl
275	183	5.8	662	2	US-09-949-016-6819	Sequence 6819, Ap	348	164	5.2	696	2	US-09-906-618-91	Sequence 91, Appl
276	183	5.8	665	2	US-09-949-016-10710	Sequence 10710, A	349	164	5.2	696	2	US-09-906-646-91	Sequence 91, Appl
277	182.5	5.8	379	2	US-09-866-028-2	Sequence 2, Appli	350	164	5.2	696	2	US-09-904-462-91	Sequence 91, Appl
278	182.5	5.8	379	2	US-09-944-457-2	Sequence 2, Appli	351	164	5.2	696	2	US-09-902-736A-91	Sequence 91, Appl
279	182.5	5.8	379	2	US-09-945-584-2	Sequence 2, Appli	352	164	5.2	696	2	US-09-906-722A-91	Sequence 91, Appl
280	182.5	5.8	379	2	US-09-944-944-2	Sequence 2, Appli	353	164	5.2	696	2	US-09-949-002-382	Sequence 382, App
281	182.5	5.8	379	2	US-09-945-587-2	Sequence 2, Appli	354	164	5.2	910	2	US-09-949-002-483	Sequence 483, App
282	182.5	5.8	958	2	US-09-706-594-5	Sequence 5, Appli	355	163	5.2	582	2	US-09-081-149-7	Sequence 7, Appli
283	182.5	5.8	966	2	US-09-964-956-32	Sequence 32, Appli	356	163	5.2	753	2	US-09-056-383-13	Sequence 13, Appli
284	182	5.8	378	2	US-09-689-486-62	Sequence 62, Appli	357	161	5.1	559	2	US-09-081-149-2	Sequence 2, Appli
285	180	5.7	493	2	US-10-037-417-30	Sequence 30, Appli	358	160	5.1	942	2	US-10-101-464A-911	Sequence 911, App
286	180	5.7	989	2	US-09-954-987B-171	Sequence 171, App	359	158.5	5.1	1032	2	US-09-954-987B-192	Sequence 192, App
287	178	5.7	368	1	US-08-303-238-3	Sequence 3, Appli	360	158	5.0	257	2	US-09-270-767-41554	Sequence 41554, A
288	178	5.7	368	2	US-08-458-834-3	Sequence 3, Appli	361	158	5.0	352	2	US-09-949-016-6781	Sequence 6781, Ap
289	178	5.7	522	2	US-09-991-181-278	Sequence 278, App	362	158	5.0	374	2	US-09-949-016-7689	Sequence 7689, Ap
290	178	5.7	522	2	US-09-990-444-278	Sequence 278, App	363	157.5	5.0	236	1	US-08-442-063A-42	Sequence 42, Appli
291	178	5.7	522	2	US-09-997-333-278	Sequence 278, App	364	157.5	5.0	672	2	US-09-949-002-522	Sequence 522, App
292	178	5.7	522	2	US-09-992-598-278	Sequence 278, App	365	157.5	5.0	796	2	US-10-104-047-2293	Sequence 2293, Ap
293	178	5.7	1049	2	US-09-999-833A-496	Sequence 496, App	366	156.5	5.0	376	2	US-09-538-092-1276	Sequence 1276, Ap
294	178	5.7	1049	2	US-09-954-987B-170	Sequence 170, App	367	156	5.0	975	2	US-09-949-016-7595	Sequence 7595, Ap
295	178	5.7	1049	2	US-10-020-445A-496	Sequence 496, App	368	155	4.9	1041	2	US-09-999-833A-498	Sequence 498, App
296	178	5.7	1052	2	US-09-949-016-11508	Sequence 11508, A	369	155	4.9	1041	2	US-09-954-987B-184	Sequence 184, App
297	177.5	5.7	1050	2	US-09-954-987B-175	Sequence 175, App	370	155	4.9	1041	2	US-09-954-987B-186	Sequence 186, App
298	176.5	5.6	522	2	US-10-104-047-2664	Sequence 2664, Ap	371	155	4.9	1041	2	US-10-020-445A-498	Sequence 498, App
299	175	5.6	368	6	5340934-2	Patent No. 5340934	372	155	4.9	1059	2	US-09-954-987B-187	Sequence 187, App
300	173.5	5.5	998	2	US-10-101-464A-914	Sequence 914, App	373	154.5	4.9	377	2	US-09-949-016-7949	Sequence 7949, Ap
301	172.5	5.5	282	1	US-08-442-063A-45	Sequence 45, Appli	374	154.5	4.9	1495	2	US-08-522-736B-1	Sequence 1, Appli
302	172.5	5.5	307	1	US-08-442-063A-48	Sequence 48, Appli	375	154.5	4.9	894	1	US-09-337-384-1	Sequence 2, Appli
303	172.5	5.5	333	1	US-08-442-063A-27	Sequence 27, Appli	376	153.5	4.9	894	1	US-08-372-892-2	Sequence 2, Appli
304	172.5	5.5	338	2	US-09-689-486-63	Sequence 63, Appli	377	153.5	4.9	894	1	US-08-445-640-34	Sequence 34, Appli
305	172.5	5.5	342	1	US-08-272-919-2	Sequence 2, Appli	378	153.5	4.9	894	2	US-08-170-558-34	Sequence 34, Appli
306	172.5	5.5	342	1	US-08-619-916-2	Sequence 2, Appli	379	153.5	4.9	894	2	US-08-447-314-34	Sequence 34, Appli
307	172.5	5.5	342	4	PCT-US95-08542-2	Sequence 2, Appli	380	153.5	4.9	894	2	US-08-445-461-34	Sequence 34, Appli
308	172.5	5.5	359	1	US-08-303-238-4	Sequence 4, Appli	381	153.5	4.9	894	2	US-09-223-490-34	Sequence 34, Appli
309	172.5	5.5	359	2	US-08-458-834-4	Sequence 4, Appli	382	153.5	4.9	1032	2	US-09-954-987B-6	Sequence 6, Appli
310	172.5	5.5	359	2	US-09-538-092-868	Sequence 868, App	383	153	4.9	679	2	US-09-252-991A-18857	Sequence 18857, A
311	172.5	5.5	359	2	US-09-949-016-6143	Sequence 6143, Ap	384	153	4.9	699	2	US-10-237-551-143	Sequence 143, App
312	172.5	5.5	360	2	US-09-949-016-7925	Sequence 7925, Ap	385	153	4.9	699	2	US-10-237-551-254	Sequence 254, App
313	172.5	5.5	1388	2	US-10-153-469A-10	Sequence 10, Appli	386	153	4.9	1248	2	US-10-042-810-2	Sequence 2, Appli
314	172.5	5.5	1388	2	US-10-104-889-10	Sequence 10, Appli	387	153	4.9	1278	2	US-10-042-810-4	Sequence 4, Appli
315	170.5	5.4	373	2	US-09-724-864-43	Sequence 43, Appli	388	152.5	4.9	364	2	US-10-104-047-2127	Sequence 2127, Ap
316	170	5.4	907	2	US-09-170-496D-264	Sequence 264, App	389	152	4.8	786	2	US-09-949-002-351	Sequence 351, App
317	170	5.4	907	2	US-09-170-496D-278	Sequence 278, App	390	152	4.8	796	2	US-09-949-002-386	Sequence 386, App
318	169.5	5.4	353	6	5340934-4	Patent No. 5340934	391	152	4.8	802	2	US-09-949-002-512	Sequence 512, App
319	168	5.4	1049	2	US-09-954-987B-172	Sequence 172, App	392	151.5	4.8	455	2	US-10-188-495-3	Sequence 3, Appli

393	151.5	4.8	1364	2	US-09-467-997-1	Sequence 1, Appli	466	138.5	4.4	811	2	US-09-997-333-57	Sequence 57, Appl
394	151	4.8	532	2	US-09-270-767-46234	Sequence 46234, A	467	138.5	4.4	811	2	US-09-992-598-57	Sequence 57, Appl
395	150.5	4.8	695	1	US-08-487-886-2	Sequence 2, Appli	468	138	4.4	323	2	US-09-949-016-7924	Sequence 7924, Ap
396	150.5	4.8	695	2	US-08-482-855-2	Sequence 2, Appli	469	137.5	4.4	141	2	US-09-270-767-45511	Sequence 45511, A
397	150.5	4.8	695	2	US-08-474-986-2	GENERAL INFO	470	137.5	4.4	884	6	5208144-8	Patent No. 5208144
398	150	4.8	259	2	US-09-907-794A-71	Sequence 71, Appl	471	137	4.4	4544	1	US-08-469-486-52	Sequence 52, Appl
399	150	4.8	259	2	US-09-905-125A-71	Sequence 71, Appl	472	137	4.4	4544	1	US-08-469-658-52	Sequence 52, Appl
400	150	4.8	259	2	US-09-902-775A-71	Sequence 71, Appl	473	136.5	4.4	984	2	US-10-101-464A-919	Sequence 919, App
401	150	4.8	259	2	US-09-906-700-71	Sequence 71, Appl	474	136.5	4.4	2972	2	US-09-579-181-2	Sequence 2, Appli
402	150	4.8	259	2	US-09-903-603A-71	Sequence 71, Appl	475	136.5	4.4	3118	2	US-09-579-181-1	Sequence 1, Appli
403	150	4.8	259	2	US-09-904-920A-71	Sequence 71, Appl	476	136	4.3	287	2	US-10-104-047-3292	Sequence 3292, Ap
404	150	4.8	259	2	US-09-909-064-71	Sequence 71, Appl	477	136	4.3	692	2	US-07-757-342D-6	Sequence 6, Appli
405	150	4.8	259	2	US-09-905-381A-71	Sequence 71, Appl	478	136	4.3	692	2	US-09-461-657B-6	Sequence 6, Appli
406	150	4.8	259	2	US-09-906-618-71	Sequence 71, Appl	479	135.5	4.3	536	2	US-09-252-931A-31124	Sequence 31124, A
407	150	4.8	259	2	US-09-906-646-71	Sequence 71, Appl	480	135.5	4.3	743	2	US-09-771-161A-164	Sequence 164, App
408	150	4.8	259	2	US-09-904-462-71	Sequence 71, Appl	481	135.5	4.3	743	2	US-09-771-161A-254	Sequence 254, App
409	150	4.8	259	2	US-09-902-736A-71	Sequence 71, Appl	482	135	4.3	446	2	US-10-101-464A-733	Sequence 733, App
410	150	4.8	259	2	US-09-906-722A-71	Sequence 71, Appl	483	135	4.3	538	2	US-09-616-289-43	Sequence 43, Appl
411	150	4.8	513	2	US-09-068-804-14	Sequence 14, Appl	484	135	4.3	538	2	US-09-976-740-43	Sequence 43, Appl
412	149	4.8	503	2	US-10-037-417-104	Sequence 104, App	485	135	4.3	723	2	US-09-434-048-2	Sequence 2, Appli
413	149	4.8	1012	1	US-08-475-891A-4	Sequence 4, Appli	486	135	4.3	723	2	US-10-104-047-2572	Sequence 2572, Ap
414	149	4.8	1025	1	US-08-567-375-4	Sequence 4, Appli	487	135	4.3	907	2	US-08-783-774-2	Sequence 2, Appli
415	149	4.8	1025	1	US-08-587-680A-4	Sequence 4, Appli	488	135	4.3	907	2	US-09-328-599A-1	Sequence 1, Appli
416	149	4.8	1026	2	US-09-623-551-18	Sequence 18, Appl	489	135	4.3	807	4	PCT-US95-04611A-19	Sequence 19, Appl
417	149	4.8	1504	2	US-09-364-206-2	Sequence 2, Appli	490	134.5	4.3	802	2	US-09-823-240A-2	Sequence 2, Appli
418	149	4.8	1874	2	US-09-331-403-2	Sequence 2, Appli	491	134	4.3	536	2	US-09-292-225-21	Sequence 21, Appl
419	148.5	4.7	375	1	US-08-303-238-2	Sequence 2, Appli	492	134	4.3	550	2	US-09-616-289-47	Sequence 47, Appl
420	148.5	4.7	375	1	US-08-458-834-2	Sequence 2, Appli	493	134	4.3	550	2	US-09-976-740-47	Sequence 47, Appl
421	147.5	4.7	570	2	US-09-565-501A-104	Sequence 104, App	494	134	4.3	555	2	US-09-292-225-15	Sequence 15, Appl
422	147.5	4.7	570	2	US-09-639-206A-104	Sequence 104, App	495	134	4.3	555	2	US-09-292-225-18	Sequence 18, Appl
423	147.5	4.7	570	2	US-09-874-923-104	Sequence 104, App	496	133.5	4.3	1166	2	US-10-101-464A-900	Sequence 900, App
424	147.5	4.7	1728	2	US-09-949-002-532	Sequence 532, App	497	133	4.2	652	2	US-10-104-047-3364	Sequence 3364, Ap
425	147	4.7	177	2	US-09-270-767-32705	Sequence 32705, A	498	133	4.2	4391	2	US-10-006-011A-2	Sequence 2, Appli
426	147	4.7	177	2	US-09-270-767-47922	Sequence 47922, A	499	132.5	4.2	390	2	US-08-460-576-2	Sequence 2, Appli
427	147	4.7	265	2	US-09-270-767-45056	Sequence 45056, A	500	132.5	4.2	463	1	US-08-162-402B-9	Sequence 9, Appli
428	147	4.7	2414	1	US-08-227-536-2	Sequence 2, Appli	501	132.5	4.2	579	2	US-09-325-932A-185	Sequence 185, App
429	147	4.7	2414	2	US-09-538-092-1289	Sequence 2, Appli	502	132.5	4.2	583	2	US-09-641-612-2	Sequence 2, Appli
430	147	4.7	2414	4	PCT-US95-04682-2	Sequence 2, Appli	503	132.5	4.2	2035	1	US-08-046-585-5	Sequence 5, Appli
431	146.5	4.7	325	2	US-10-104-047-3320	Sequence 3320, Ap	504	132.5	4.2	2035	1	US-08-393-703-5	Sequence 5, Appli
432	146.5	4.7	344	2	US-10-104-047-3358	Sequence 3358, Ap	505	132.5	4.2	2035	4	PCT-US93-11721-5	Sequence 5, Appli
433	146.5	4.7	1404	1	US-08-400-159-2	Sequence 2, Appli	506	132.5	4.2	2045	2	US-09-949-016-10491	Sequence 10491, A
434	146.5	4.7	1404	2	US-08-611-729A-2	Sequence 2, Appli	507	132.5	4.2	3122	2	US-10-237-551-201	Sequence 201, App
435	146.5	4.7	1404	2	US-09-195-524-2	Sequence 2, Appli	508	132.5	4.2	3122	2	US-10-237-551-250	Sequence 250, App
436	146	4.7	786	2	US-09-103-429A-3	Sequence 3, Appli	509	132	4.2	287	2	US-09-893-737-110	Sequence 110, App
437	146	4.7	788	2	US-09-294-663-3	Sequence 3, Appli	510	132	4.2	465	1	US-08-162-402B-8	Sequence 8, Appli
438	146	4.7	885	1	US-08-372-892-4	Sequence 4, Appli	511	132	4.2	705	2	US-10-101-464A-894	Sequence 894, App
439	146	4.7	885	2	US-09-919-497-52	Sequence 52, Appl	512	132	4.2	979	2	US-08-514-213A-2	Sequence 2, Appli
440	145.5	4.6	2142	2	US-09-538-092-1142	Sequence 1142, Ap	513	132	4.2	979	2	US-09-949-016-11260	Sequence 11260, A
441	145.5	4.6	2142	2	US-09-949-002-371	Sequence 371, App	514	132	4.2	1003	2	US-09-437-417-96	Sequence 96, Appl
442	145	4.6	353	2	US-09-949-016-7923	Sequence 7923, Ap	515	131.5	4.2	461	2	US-10-037-417-96	Sequence 96, Appl
443	145	4.6	1032	2	US-09-954-987B-3	Sequence 3, Appli	516	131.5	4.2	571	2	US-09-252-991A-30533	Sequence 30533, A
444	144	4.6	661	1	US-08-514-014-4	Sequence 4, Appli	517	131	4.2	180	2	US-08-986-485-8	Sequence 8, Appli
445	144	4.6	661	1	US-08-833-823-4	Sequence 4, Appli	518	131	4.2	227	2	US-10-101-464A-666	Sequence 666, App
446	143.5	4.6	1274	2	US-09-095-443-2	Sequence 2, Appli	519	131	4.2	279	2	US-09-270-767-41558	Sequence 41558, A
447	143	4.6	935	2	US-09-477-962-107	Sequence 107, App	520	131	4.2	407	2	US-09-270-767-46649	Sequence 6, Appli
448	142.5	4.5	141	2	US-09-270-767-31706	Sequence 31706, A	521	131	4.2	799	2	US-09-180-439-6	Sequence 6, Appli
449	142.5	4.5	141	2	US-09-270-767-46923	Sequence 46923, A	522	131	4.2	947	2	US-09-228-986-73	Sequence 73, Appl
450	142.5	4.5	805	2	US-09-103-429A-4	Sequence 4, Appli	523	131	4.2	947	2	US-10-101-464A-73	Sequence 73, Appl
451	142.5	4.5	807	2	US-09-294-663-4	Sequence 4, Appli	524	131	4.2	1062	2	US-09-902-540-16313	Sequence 16313, A
452	142	4.5	363	2	US-09-689-486-64	Sequence 64, Appl	525	131	4.2	1196	2	US-08-881-706-2	Sequence 2, Appli
453	142	4.5	363	2	US-10-188-495-6	Sequence 6, Appli	526	131	4.2	1196	2	US-09-823-394-2	Sequence 2, Appli
454	142	4.5	365	2	US-10-101-464A-901	Sequence 901, App	527	131	4.2	1938	2	US-09-949-016-6609	Sequence 6609, Ap
455	142	4.5	435	2	US-10-188-495-5	Sequence 5, Appli	528	130.5	4.2	843	2	US-10-101-464A-893	Sequence 893, App
456	142	4.5	661	2	US-10-037-417-107	Sequence 107, App	529	130.5	4.2	878	2	US-09-556-706B-2	Sequence 2, Appli
457	140.5	4.5	345	2	US-10-101-464A-802	Sequence 802, App	530	130.5	4.2	878	2	US-09-724-418A-2	Sequence 2, Appli
458	140.5	4.5	376	1	US-08-303-238-1	Sequence 1, Appli	531	130.5	4.2	3729	1	US-08-804-227C-4	Sequence 4, Appli
459	140.5	4.5	376	2	US-08-458-834-1	Sequence 1, Appli	532	130	4.1	619	2	US-10-037-417-34	Sequence 34, Appl
460	140	4.5	283	2	US-09-949-016-7910	Sequence 7910, Ap	533	130	4.1	645	2	US-10-101-464A-920	Sequence 920, App
461	140	4.5	547	2	US-10-101-464A-928	Sequence 928, App	534	129.5	4.1	550	2	US-09-252-991A-21295	Sequence 21295, A
462	139	4.4	5179	2	US-09-538-092-1258	Sequence 1258, Ap	535	129.5	4.1	912	4	PCT-US95-03747-2	Sequence 2, Appli
463	138.5	4.4	710	2	US-10-104-047-3402	Sequence 3402, Ap	536	129	4.1	363	2	US-09-270-767-44030	Sequence 44030, A
464	138.5	4.4	811	2	US-09-991-181-57	Sequence 57, Appl	537	129	4.1	823	2	US-09-252-991A-23655	Sequence 23655, A
465	138.5	4.4	811	2	US-09-990-444-57	Sequence 57, Appl	538	129	4.1	885	2	US-09-252-991A-26129	Sequence 26129, A

539	129	4.1	1133	2	US-10-101-464A-809	Sequence 809, App	612	124.5	4.0	546	2	US-09-906-700-250	Sequence 250, App
540	129	4.1	1940	1	US-08-644-271-30	Sequence 30, Appl	613	124.5	4.0	546	2	US-09-903-603A-250	Sequence 250, App
541	129	4.1	1940	1	US-09-077-955-34	Sequence 34, Appl	614	124.5	4.0	546	2	US-09-904-920A-250	Sequence 250, App
542	129	4.1	1940	2	US-10-016-283-34	Sequence 34, Appl	615	124.5	4.0	546	2	US-09-909-064-250	Sequence 250, App
543	129	4.1	2321	2	US-09-230-652-2	Sequence 2, Appl	616	124.5	4.0	546	2	US-09-905-381A-250	Sequence 250, App
544	128.5	4.1	188	1	US-08-442-063A-39	Sequence 39, Appl	617	124.5	4.0	546	2	US-09-906-618-250	Sequence 250, App
545	128.5	4.1	446	1	US-08-836-854-15	Sequence 15, Appl	618	124.5	4.0	546	2	US-09-906-646-250	Sequence 250, App
546	128.5	4.1	508	2	US-10-104-047-3233	Sequence 3233, Ap	619	124.5	4.0	546	2	US-09-904-462-250	Sequence 250, App
547	128.5	4.1	653	2	US-10-101-464A-953	Sequence 953, App	620	124.5	4.0	546	2	US-09-902-736A-250	Sequence 250, App
548	128.5	4.1	864	2	US-10-101-464A-896	Sequence 896, App	621	124.5	4.0	546	2	US-09-906-722A-250	Sequence 250, App
549	128.5	4.1	865	2	US-09-902-540-10416	Sequence 10416, A	622	124.5	4.0	623	2	US-09-949-016-6330	Sequence 6330, Ap
550	128.5	4.1	1023	1	US-08-475-891A-2	Sequence 2, Appl	623	124.5	4.0	998	2	US-10-101-464A-895	Sequence 895, App
551	128.5	4.1	1023	1	US-08-567-375-2	Sequence 2, Appl	624	124.5	4.0	1042	2	US-09-252-991A-30444	Sequence 30444, A
552	128.5	4.1	1023	1	US-08-587-680A-2	Sequence 2, Appl	625	124.5	4.0	1709	2	US-09-949-016-10503	Sequence 10503, A
553	128	4.1	475	2	US-09-252-991A-30242	Sequence 30242, A	626	124	4.0	277	2	US-07-741-453A-58	Sequence 58, Appl
554	128	4.1	538	1	US-08-541-759B-2	Sequence 2, Appl	627	124	4.0	707	2	US-09-228-986-80	Sequence 80, Appl
555	128	4.1	717	2	US-10-101-464A-810	Sequence 810, App	628	124	4.0	707	2	US-10-101-464A-80	Sequence 80, Appl
556	127.5	4.1	1006	2	US-10-415-147-12	Sequence 12, Appl	629	124	4.0	1457	2	US-08-665-253-27	Sequence 27, Appl
557	127.5	4.1	1522	2	US-10-144-198-31	Sequence 31, Appl	630	124	4.0	1457	2	US-08-762-500-27	Sequence 27, Appl
558	127.5	4.1	1581	2	US-09-949-002-414	Sequence 414, App	631	124	4.0	1472	2	US-09-032-438C-119	Sequence 119, App
559	127.5	4.1	3969	2	US-08-061-376-5	Sequence 5, Appl	632	123.5	3.9	1312	2	US-09-041-886-19	Sequence 19, Appl
560	127.5	4.1	3969	2	US-09-538-092-1262	Sequence 1262, Ap	633	123.5	3.9	1312	2	US-09-648-281-2	Sequence 2, Appl
561	127	4.1	260	2	US-09-270-767-32658	Sequence 32658, A	634	123.5	3.9	1312	2	US-09-707-919A-19	Sequence 19, Appl
562	127	4.1	615	2	US-09-252-991A-26695	Sequence 26695, A	635	123.5	3.9	1312	2	US-09-083-268-3	Sequence 3, Appl
563	126.5	4.0	141	2	US-09-270-767-32244	Sequence 32244, A	636	123.5	3.9	1312	2	US-08-981-998A-3	Sequence 3, Appl
564	126.5	4.0	141	2	US-09-270-767-47461	Sequence 47461, A	637	123	3.9	383	2	US-10-101-464A-898	Sequence 898, App
565	126.5	4.0	438	2	US-09-991-181-129	Sequence 129, App	638	123	3.9	526	2	US-09-252-991A-23688	Sequence 23688, A
566	126.5	4.0	438	2	US-09-990-444-129	Sequence 129, App	639	123	3.9	557	2	US-09-248-796A-26892	Sequence 26892, A
567	126.5	4.0	438	2	US-09-997-333-129	Sequence 129, App	640	123	3.9	888	1	US-08-445-640-35	Sequence 35, Appl
568	126.5	4.0	438	2	US-09-992-598-129	Sequence 129, App	641	123	3.9	888	2	US-08-170-558-35	Sequence 35, Appl
569	126.5	4.0	659	2	US-09-423-753-3	Sequence 3, Appl	642	123	3.9	888	2	US-08-447-314-35	Sequence 35, Appl
570	126.5	4.0	685	2	US-08-872-855-2	Sequence 2, Appl	643	123	3.9	888	2	US-08-445-461-35	Sequence 35, Appl
571	126.5	4.0	685	2	US-09-423-753-25	Sequence 25, Appl	644	123	3.9	888	2	US-09-223-490-35	Sequence 35, Appl
572	126.5	4.0	685	2	US-09-641-612-7	Sequence 7, Appl	645	123	3.9	924	1	US-08-481-130-28	Sequence 28, Appl
573	126.5	4.0	919	2	US-10-101-464A-642	Sequence 642, App	646	123	3.9	924	1	US-08-656-984A-28	Sequence 28, Appl
574	126.5	4.0	999	1	US-08-473-553A-5	Sequence 5, Appl	647	123	3.9	924	1	US-08-485-604-28	Sequence 28, Appl
575	126	4.0	143	2	US-09-893-737-190	Sequence 190, App	648	123	3.9	924	1	US-08-487-595-28	Sequence 28, Appl
576	126	4.0	152	2	US-09-270-767-33594	Sequence 33594, A	649	122.5	3.9	494	2	US-09-248-796A-16546	Sequence 16546, A
577	126	4.0	775	2	US-09-949-016-8799	Sequence 8799, Ap	650	122.5	3.9	585	2	US-09-641-612-5	Sequence 5, Appl
578	126	4.0	1485	2	US-09-762-569-4	Sequence 4, Appl	651	122.5	3.9	596	2	US-09-252-991A-18875	Sequence 18875, A
579	126	4.0	1821	2	US-09-949-016-5938	Sequence 5938, Ap	652	122.5	3.9	968	2	US-09-180-439-3	Sequence 3, Appl
580	125.5	4.0	258	2	US-10-012-231A-153	Sequence 153, App	653	122.5	3.9	968	2	US-09-180-439-3	Sequence 3, Appl
581	125.5	4.0	258	2	US-10-015-389A-153	Sequence 153, App	654	122.5	3.9	1016	2	US-09-180-439-8	Sequence 8, Appl
582	125.5	4.0	258	2	US-10-006-768A-153	Sequence 153, App	655	122.5	3.9	1036	2	US-09-771-161A-255	Sequence 255, App
583	125.5	4.0	258	2	US-10-015-671A-153	Sequence 153, App	656	122.5	3.9	1036	2	US-09-771-161A-256	Sequence 256, App
584	125.5	4.0	258	2	US-10-015-393A-153	Sequence 153, App	657	122	3.9	191	2	US-09-461-325-186	Sequence 186, App
585	125.5	4.0	258	2	US-10-011-833A-153	Sequence 153, App	658	122	3.9	191	2	US-10-012-542-186	Sequence 186, App
586	125.5	4.0	258	2	US-10-006-041A-153	Sequence 153, App	659	122	3.9	191	2	US-10-115-123-186	Sequence 186, App
587	125.5	4.0	258	2	US-10-012-064A-153	Sequence 153, App	660	122	3.9	206	2	US-09-461-325-412	Sequence 412, App
588	125.5	4.0	440	2	US-08-985-335-3	Sequence 3, Appl	661	122	3.9	206	2	US-10-115-123-412	Sequence 412, App
589	125.5	4.0	440	2	US-09-410-372-3	Sequence 3, Appl	662	122	3.9	312	2	US-09-270-767-31750	Sequence 31750, A
590	125.5	4.0	764	2	US-07-741-453A-54	Sequence 54, Appl	663	122	3.9	328	1	US-08-414-928A-9	Sequence 9, Appl
591	125.5	4.0	764	2	US-07-741-453A-60	Sequence 60, Appl	664	122	3.9	328	1	US-08-926-922-9	Sequence 9, Appl
592	125.5	4.0	1129	2	US-09-023-905A-2	Sequence 2, Appl	665	122	3.9	328	1	US-09-253-682-9	Sequence 9, Appl
593	125	4.0	419	2	US-10-002-344A-237	Sequence 237, App	666	122	3.9	328	2	US-09-527-657-9	Sequence 9, Appl
594	125	4.0	757	2	US-09-252-991A-25918	Sequence 25918, A	667	122	3.9	328	2	US-09-892-100-9	Sequence 9, Appl
595	125	4.0	957	2	US-09-252-991A-20408	Sequence 20408, A	668	122	3.9	481	2	US-09-949-016-9748	Sequence 9748, Ap
596	125	4.0	1139	2	US-09-513-505-2	Sequence 8, Appl	669	122	3.9	495	2	US-09-252-991A-31949	Sequence 31949, A
597	125	4.0	2023	2	US-09-491-356C-8	Sequence 8, Appl	670	122	3.9	517	2	US-09-252-991A-28127	Sequence 28127, A
598	125	4.0	2026	2	US-09-487-558B-86	Sequence 86, Appl	671	122	3.9	527	2	US-09-370-83A-216	Sequence 216, App
599	125	4.0	2124	2	US-09-538-092-1377	Sequence 1377, Ap	672	122	3.9	527	2	US-09-854-133-216	Sequence 216, App
600	125	4.0	2294	2	US-09-252-991A-17231	Sequence 17231, A	673	122	3.9	529	2	US-09-716-9648-2	Sequence 2, Appl
601	124.5	4.0	107	2	US-09-270-767-61021	Sequence 61021, A	674	122	3.9	529	2	US-09-325-932A-190	Sequence 190, App
602	124.5	4.0	298	2	US-09-232-160-17	Sequence 17, Appl	675	121.5	3.9	320	2	US-09-252-991A-19831	Sequence 19831, A
603	124.5	4.0	298	2	US-09-800-729-87	Sequence 87, Appl	676	121.5	3.9	477	2	US-09-248-796A-18020	Sequence 18020, A
604	124.5	4.0	298	2	US-09-800-729-121	Sequence 121, App	677	121.5	3.9	695	2	US-10-104-047-2546	Sequence 2546, Ap
605	124.5	4.0	298	2	US-10-000-489-22	Sequence 22, Appl	678	121.5	3.9	818	2	US-10-501-171-4	Sequence 4, Appl
606	124.5	4.0	298	2	US-09-832-129-50	Sequence 50, Appl	679	121.5	3.9	1225	2	US-09-949-016-6063	Sequence 6063, Ap
607	124.5	4.0	307	2	US-09-949-016-9817	Sequence 9817, Ap	680	121.5	3.9	1225	2	PCT-US95-02251-3	Sequence 3, Appl
608	124.5	4.0	307	2	US-09-949-016-9818	Sequence 9818, Ap	681	121.5	3.9	1251	4	US-08-199-780-3	Sequence 3, Appl
609	124.5	4.0	546	2	US-09-907-794A-250	Sequence 250, App	682	121.5	3.9	1252	1	US-08-316-650-3	Sequence 3, Appl
610	124.5	4.0	546	2	US-09-905-125A-250	Sequence 250, App	683	121.5	3.9	1252	1	US-08-479-722B-4	Sequence 4, Appl
611	124.5	4.0	546	2	US-09-902-775A-250	Sequence 250, App	684	121.5	3.9	1253	2		

685	121.5	3.9	1253	2	US-09-592-685-4	Sequence 4, Appli	758	117.5	3.7	190	1	US-08-441-629-4	Sequence 4, Appli
686	121	3.9	499	2	US-09-049-672A-1	Sequence 1, Appli	759	117.5	3.7	190	2	US-08-776-207-4	Sequence 4, Appli
687	121	3.9	739	2	US-09-902-540-10606	Sequence 10606, A	760	117.5	3.7	190	2	US-09-507-773-4	Sequence 4, Appli
688	121	3.9	910	2	US-09-228-986-72	Sequence 72, Appl	761	117.5	3.7	190	2	US-10-016-447-4	Sequence 4, Appli
689	121	3.9	910	2	US-10-101-464A-72	Sequence 72, Appl	762	117.5	3.7	190	4	PCT-US95-09172-4	Sequence 4, Appli
690	121	3.9	1139	2	US-09-513-503-4	Sequence 4, Appli	763	117.5	3.7	247	2	US-10-101-464A-730	Sequence 730, App
691	120.5	3.8	141	1	US-08-442-063A-36	Sequence 36, Appl	764	117.5	3.7	563	2	US-09-252-991A-17549	Sequence 17549, A
692	120.5	3.8	426	2	US-09-252-991A-24450	Sequence 24450, A	765	117.5	3.7	635	1	US-08-484-101B-36	Sequence 36, Appl
693	120.5	3.8	464	2	US-09-716-964B-4	Sequence 4, Appli	766	117.5	3.7	635	1	US-08-484-101B-50	Sequence 50, Appl
694	120.5	3.8	562	2	US-09-902-540-13269	Sequence 13269, A	767	117.5	3.7	635	2	US-08-714-524D-36	Sequence 36, Appl
695	120.5	3.8	787	2	US-09-721-383-2	Sequence 2, Appli	768	117.5	3.7	635	2	US-08-714-524D-50	Sequence 50, Appl
696	120.5	3.8	787	2	US-09-721-137-2	Sequence 2, Appli	769	117.5	3.7	996	2	US-10-101-464A-889	Sequence 889, App
697	120.5	3.8	787	2	US-09-721-251-2	Sequence 2, Appli	770	117.5	3.7	996	2	US-10-101-464A-933	Sequence 933, App
698	120.5	3.8	787	2	US-10-114-764-2	Sequence 2, Appli	771	117.5	3.7	1118	1	US-09-252-991A-24340	Sequence 24340, A
699	120.5	3.8	988	2	US-10-101-464A-931	Sequence 931, App	772	117.5	3.7	1706	1	US-08-459-588-2	Sequence 2, Appli
700	120.5	3.8	1104	2	US-09-981-953A-4	Sequence 4, Appli	773	117.5	3.7	1706	1	US-08-399-411-2	Sequence 2, Appli
701	120.5	3.8	1587	2	US-09-949-002-354	Sequence 354, App	774	117.5	3.7	1706	2	US-08-516-859A-2	Sequence 2, Appli
702	120.5	3.8	1610	2	US-09-548-473B-4	Sequence 4, Appli	775	117.5	3.7	1706	2	US-09-586-472-2	Sequence 2, Appli
703	120.5	3.8	1665	2	US-09-858-664A-2	Sequence 2, Appli	776	117.5	3.7	1706	2	US-09-528-706-2	Sequence 2, Appli
704	120.5	3.8	1665	2	US-10-274-978-2	Sequence 2, Appli	777	117.5	3.7	1706	2	US-10-024-450-2	Sequence 2, Appli
705	120.5	3.8	1665	2	US-10-697-263-2	Sequence 2, Appli	778	117	3.7	401	2	US-09-252-991A-32529	Sequence 32529, A
706	120.5	3.8	2396	2	US-09-548-473B-6	Sequence 6, Appli	779	117	3.7	655	1	US-08-148-910-12	Sequence 12, Appl
707	120	3.8	130	2	US-09-270-767-33086	Sequence 33086, A	780	117	3.7	655	1	US-08-448-937A-12	Sequence 12, Appl
708	120	3.8	467	2	US-09-046-736-2	Sequence 2, Appli	781	117	3.7	809	2	US-09-252-991A-31759	Sequence 31759, A
709	120	3.8	523	1	US-08-473-553A-3	Sequence 3, Appli	782	117	3.7	888	2	US-09-252-991A-23787	Sequence 23787, A
710	120	3.8	569	2	US-09-514-245-22	Sequence 22, Appl	783	117	3.7	980	1	US-08-473-553A-6	Sequence 6, Appli
711	120	3.8	603	2	US-09-506-779-4	Sequence 4, Appli	784	117	3.7	985	1	US-08-473-553A-2	Sequence 2, Appli
712	120	3.8	696	2	US-09-758-759-125	Sequence 125, App	785	117	3.7	1055	2	US-09-214-278-2	Sequence 2, Appli
713	120	3.8	2556	1	US-08-185-432-17	Sequence 17, Appl	786	117	3.7	1055	2	US-08-855-722-2	Sequence 2, Appli
714	120	3.8	2556	2	US-08-899-232-2	Sequence 2, Appli	787	117	3.7	1148	2	US-08-882-046-4	Sequence 4, Appli
715	120	3.8	2556	2	US-09-121-457-2	Sequence 2, Appli	788	117	3.7	1148	2	US-09-566-047-4	Sequence 4, Appli
716	120	3.8	2556	2	US-09-107-433-3721	Sequence 3721, Ap	789	117	3.7	1193	1	US-08-400-159-10	Sequence 10, Appl
717	119.5	3.8	608	2	US-09-949-016-11148	Sequence 11148, A	790	117	3.7	1193	2	US-08-611-729A-10	Sequence 10, Appl
718	119.5	3.8	608	2	US-09-949-016-11149	Sequence 11149, A	791	117	3.7	1193	2	US-09-195-524-10	Sequence 10, Appl
719	119.5	3.8	608	2	US-09-949-016-11150	Sequence 11150, A	792	117	3.7	1193	2	US-09-310-685-8	Sequence 8, Appli
720	119.5	3.8	608	2	US-09-949-016-11150	Sequence 11150, A	793	117	3.7	1212	2	US-09-214-278-3	Sequence 3, Appli
721	119.5	3.8	608	2	US-09-949-016-11151	Sequence 11151, A	794	117	3.7	1212	2	US-09-855-722-3	Sequence 3, Appli
722	119.5	3.8	1034	2	US-09-252-991A-28921	Sequence 28921, A	795	117	3.7	1238	2	US-09-214-278-5	Sequence 5, Appli
723	119.5	3.8	1048	2	US-09-171-699-10	Sequence 10, Appl	796	117	3.7	1238	2	US-09-855-722-5	Sequence 5, Appli
724	119.5	3.8	1149	2	US-08-560-005-5	Sequence 5, Appli	797	117	3.7	1257	2	US-08-611-729A-8	Sequence 8, Appli
725	119.5	3.8	1149	2	US-09-418-540-5	Sequence 5, Appli	798	117	3.7	1257	2	US-09-195-524-8	Sequence 8, Appli
726	119.5	3.8	1149	2	US-09-969-528-5	Sequence 5, Appli	799	117	3.7	1257	2	US-09-310-685-6	Sequence 6, Appli
727	119.5	3.8	1596	2	US-09-538-092-887	Sequence 887, App	800	116.5	3.7	132	2	US-10-101-464A-572	Sequence 572, App
728	119	3.8	304	2	US-10-101-464A-717	Sequence 717, App	801	116.5	3.7	296	2	US-09-270-767-37980	Sequence 37980, A
729	119	3.8	319	2	US-08-630-172-12	Sequence 12, Appl	802	116.5	3.7	296	2	US-09-270-767-53197	Sequence 53197, A
730	119	3.8	319	2	US-09-375-413-12	Sequence 12, Appl	803	116.5	3.7	439	2	US-10-300-819B-21	Sequence 21, Appl
731	119	3.8	528	2	US-08-928-213B-8	Sequence 8, Appli	804	116.5	3.7	943	2	US-08-476-515A-12	Sequence 12, Appl
732	119	3.8	593	2	US-09-252-991A-20441	Sequence 20441, A	805	116.5	3.7	944	2	US-08-652-877-12	Sequence 12, Appl
733	119	3.8	784	2	US-09-982-308B-23	Sequence 23, Appl	806	116.5	3.7	1252	2	US-09-902-540-13967	Sequence 13967, A
734	119	3.8	1081	2	US-09-369-364A-17	Sequence 17, Appl	807	116.5	3.7	2887	2	US-08-462-467B-8	Sequence 8, Appli
735	118.5	3.8	171	2	US-09-270-767-43049	Sequence 43049, A	808	116.5	3.7	4654	2	US-08-476-515A-84	Sequence 84, Appli
736	118.5	3.8	422	2	US-09-949-016-8251	Sequence 8251, Ap	809	116.5	3.7	4655	2	US-08-652-877-84	Sequence 84, Appl
737	118.5	3.8	430	2	US-09-949-016-8782	Sequence 8782, Ap	810	116.5	3.7	4655	2	US-08-652-877-86	Sequence 86, Appl
738	118.5	3.8	486	1	US-08-450-360-2	Sequence 2, Appli	811	116.5	3.7	4655	2	US-08-652-877-88	Sequence 88, Appl
739	118.5	3.8	883	2	US-10-188-495-72	Sequence 72, Appl	812	116.5	3.7	4655	2	US-08-652-877-90	Sequence 90, Appl
740	118.5	3.8	1166	2	US-10-104-047-2949	Sequence 2949, Ap	813	116	3.7	193	2	US-09-270-767-44942	Sequence 44942, A
741	118.5	3.8	1321	1	US-08-317-310A-64	Sequence 64, Appl	814	116	3.7	264	2	US-09-252-991A-24670	Sequence 24670, A
742	118	3.8	149	2	US-09-270-767-32618	Sequence 32618, A	815	116	3.7	1053	2	US-09-513-505-8	Sequence 8, Appli
743	118	3.8	149	2	US-09-270-767-47835	Sequence 47835, A	816	116	3.7	1181	2	US-09-826-509-587	Sequence 587, App
744	118	3.8	462	2	US-09-252-991A-20814	Sequence 20814, A	817	116	3.7	1291	2	US-09-150-460B-10	Sequence 10, Appl
745	118	3.8	947	2	US-09-252-991A-21335	Sequence 21335, A	818	116	3.7	1291	2	US-09-220-641-5	Sequence 5, Appli
746	118	3.8	1044	2	US-09-252-991A-18853	Sequence 18853, A	819	116	3.7	1251	2	US-09-548-473B-1	Sequence 1, Appli
747	118	3.8	1064	2	US-09-252-991A-17508	Sequence 17508, A	820	116	3.7	2556	1	US-08-083-550A-20	Sequence 20, Appl
748	118	3.8	1084	2	US-09-227-725A-3	Sequence 3, Appli	821	116	3.7	2556	2	US-08-532-384-20	Sequence 20, Appl
749	118	3.8	1084	2	US-10-071-900-3	Sequence 3, Appli	822	115.5	3.7	138	2	US-09-191-647-4	Sequence 4, Appli
750	118	3.8	1864	1	US-08-804-227C-3	Sequence 3, Appli	823	115.5	3.7	138	2	US-09-540-245A-4	Sequence 4, Appli
751	118	3.8	2471	1	US-08-185-432-16	Sequence 16, Appl	824	115.5	3.7	138	2	US-09-540-153-4	Sequence 4, Appli
752	118	3.8	2471	1	US-08-083-590A-19	Sequence 19, Appl	825	115.5	3.7	138	2	US-10-289-776-4	Sequence 4, Appli
753	118	3.8	2471	2	US-08-532-384-19	Sequence 19, Appl	826	115.5	3.7	412	2	US-09-252-991A-24484	Sequence 24484, A
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756	117.5	3.7	129	2	US-09-513-999C-4304	Sequence 4304, Ap	829	115.5	3.7	1093	4	PCT-US94-04496-55	Sequence 55, Appl
757	117.5	3.7	189	2	US-10-101-464A-517	Sequence 517, App	830	115	3.7	305	2	US-09-325-932A-188	Sequence 188, App

831	115	3.7	447	1	US-08-450-360-4	Sequence 4, Appli	904	113	3.6	681	2	US-10-362-247-2	Sequence 2, Appli
832	115	3.7	764	2	US-07-741-453A-59	Sequence 59, Appl	905	113	3.6	688	2	US-09-367-206-20	Sequence 20, Appl
833	115	3.7	764	2	US-07-741-453A-61	Sequence 61, Appl	906	113	3.6	688	2	US-09-298-404-20	Sequence 20, Appl
834	115	3.7	984	2	US-09-287-354-2	Sequence 2, Appli	907	113	3.6	723	2	US-10-104-047-2246	Sequence 2246, Ap
835	115	3.7	1053	2	US-09-513-505-6	Sequence 6, Appli	908	113	3.6	770	2	US-09-981-953A-2	Sequence 2, Appli
836	115	3.7	1033	2	US-09-252-991A-21827	Sequence 21827, A	909	113	3.6	979	2	US-09-538-092-990	Sequence 990, App
837	115	3.7	1189	2	US-09-287-354-4	Sequence 4, Appli	910	113	3.6	1247	2	US-09-501-171-6	Sequence 6, Appli
838	115	3.7	1189	2	US-09-949-016-6931	Sequence 6931, Ap	911	112.5	3.6	328	2	US-09-252-991A-17729	Sequence 17729, A
839	115	3.7	1219	2	US-08-882-046-5	Sequence 5, Appli	912	112.5	3.6	677	1	US-08-188-583-13	Sequence 13, Appl
840	115	3.7	1219	2	US-09-566-047-5	Sequence 5, Appli	913	112.5	3.6	677	1	US-08-646-715-13	Sequence 13, Appl
841	115	3.7	2415	2	US-09-949-002-398	Sequence 398 App	914	112.5	3.6	677	2	US-09-538-092-1164	Sequence 1164, Ap
842	114.5	3.7	166	2	US-09-270-767-59438	Sequence 59438, A	915	112.5	3.6	694	2	US-09-949-016-8774	Sequence 8774, Ap
843	114.5	3.7	545	2	US-09-949-002-297	Sequence 297, App	916	112.5	3.6	694	2	US-09-949-016-8775	Sequence 8775, Ap
844	114.5	3.7	545	2	US-09-509-595B-2	Sequence 2, Appli	917	112.5	3.6	711	2	US-09-949-016-8493	Sequence 8493, Ap
845	114.5	3.7	545	2	US-09-509-595B-8	Sequence 8, Appli	918	112.5	3.6	1068	1	US-08-396-479B-12	Sequence 12, Appl
846	114.5	3.7	587	2	US-09-949-016-8708	Sequence 8708, Ap	919	112.5	3.6	1068	1	US-08-818-823-12	Sequence 12, Appl
847	114.5	3.7	587	2	US-09-949-016-8709	Sequence 8709, Ap	920	112.5	3.6	1078	2	US-09-949-016-9573	Sequence 9573, Ap
848	114.5	3.7	587	2	US-09-949-002-461	Sequence 461, App	921	112	3.6	230	2	US-09-252-991A-31737	Sequence 31737, A
849	114.5	3.7	661	2	US-09-949-016-9121	Sequence 9121, App	922	112	3.6	241	2	US-08-341-018-54	Sequence 54, Appl
850	114.5	3.7	804	2	US-10-101-464A-890	Sequence 890, App	923	112	3.6	241	2	US-08-470-339-195	Sequence 195, App
851	114.5	3.7	935	2	US-09-902-540-16200	Sequence 16200, A	924	112	3.6	241	2	US-08-470-339-195	Sequence 195, App
852	114.5	3.7	1010	2	US-08-882-046-7	Sequence 7, Appli	925	112	3.6	241	2	US-08-467-602-389	Sequence 389, App
853	114.5	3.7	1010	2	US-09-566-047-7	Sequence 7, Appli	926	112	3.6	241	2	US-08-411-295F-47	Sequence 47, Appl
854	114.5	3.7	1017	2	US-09-600-776-6	Sequence 6, Appli	927	112	3.6	241	2	US-08-411-295F-94	Sequence 94, Appl
855	114.5	3.7	1017	2	US-09-965-830-6	Sequence 6, Appli	928	112	3.6	297	1	US-08-580-545B-6	Sequence 6, Appli
856	114.5	3.7	1036	2	US-09-668-740A-6	Sequence 6, Appli	929	112	3.6	297	1	US-09-262-653A-6	Sequence 6, Appli
857	114.5	3.7	1036	2	US-09-579-536C-18	Sequence 18, Appl	930	112	3.6	383	1	US-08-597-545-2	Sequence 2, Appli
858	114.5	3.7	1162	1	US-08-728-323A-2	Sequence 2, Appli	931	112	3.6	383	1	US-08-457-135-2	Sequence 2, Appli
859	114.5	3.7	1162	2	US-09-298-568-2	Sequence 2, Appli	932	112	3.6	383	2	US-09-142-027A-12	Sequence 12, Appl
860	114.5	3.7	1162	2	US-09-410-399-2	Sequence 2, Appli	933	112	3.6	388	2	US-09-644-858-11	Sequence 11, Appl
861	114.5	3.7	1162	2	US-09-894-273-2	Sequence 2, Appli	934	112	3.6	417	2	US-09-644-858-5	Sequence 5, Appli
862	114.5	3.7	1187	2	US-09-068-740A-7	Sequence 7, Appli	935	112	3.6	417	2	US-09-644-858-8	Sequence 8, Appli
863	114.5	3.7	1208	2	US-09-199-865-1	Sequence 1, Appli	936	112	3.6	422	2	US-09-644-858-13	Sequence 13, Appl
864	114.5	3.7	1208	2	US-10-213-329-1	Sequence 1, Appli	937	112	3.6	479	2	US-09-252-991A-23144	Sequence 23144, A
865	114.5	3.7	1218	1	US-08-400-159-6	Sequence 6, Appli	938	112	3.6	513	1	US-08-480-228C-14	Sequence 14, Appl
866	114.5	3.7	1218	2	US-08-611-729A-6	Sequence 6, Appli	939	112	3.6	513	1	US-08-659-235C-14	Sequence 14, Appl
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869	114.5	3.7	1218	2	US-09-566-047-2	Sequence 2, Appli	942	112	3.6	764	2	US-07-757-342D-5	Sequence 5, Appli
870	114.5	3.7	1218	2	US-09-917-254-85	Sequence 85, Appl	943	112	3.6	764	2	US-09-461-657B-5	Sequence 5, Appli
871	114.5	3.7	1218	2	US-09-195-524-6	Sequence 6, Appli	944	112	3.6	764	2	US-09-826-509-395	Sequence 395, App
872	114.5	3.7	1218	2	US-09-579-536C-1	Sequence 1, Appli	945	112	3.6	764	2	US-09-826-509-399	Sequence 399, App
873	114.5	3.7	1218	2	US-09-949-016-5902	Sequence 5902, Ap	946	112	3.6	764	2	US-09-826-509-403	Sequence 403, App
874	114.5	3.7	1218	2	US-09-310-685-4	Sequence 4, Appli	947	112	3.6	764	2	US-09-826-509-407	Sequence 407, App
875	114.5	3.7	1254	2	US-09-949-016-10297	Sequence 10297, A	948	112	3.6	764	2	US-09-826-509-411	Sequence 411, App
876	114.5	3.7	2169	2	US-09-949-016-6930	Sequence 6930, Ap	949	112	3.6	764	2	US-09-826-509-415	Sequence 415, App
877	114	3.6	111	2	US-09-220-528-53	Sequence 53, Appl	950	112	3.6	764	2	US-09-826-509-419	Sequence 419, App
878	114	3.6	224	2	US-09-347-613C-16	Sequence 16, Appl	951	112	3.6	764	2	US-08-396-479B-6	Sequence 6, Appli
879	114	3.6	224	2	US-09-347-613C-16	Sequence 16, Appl	952	112	3.6	902	1	US-08-818-823-6	Sequence 6, Appli
880	114	3.6	224	2	US-10-101-464A-743	Sequence 743, App	953	112	3.6	902	1	US-10-101-464A-814	Sequence 814, App
881	114	3.6	257	2	US-10-101-464A-743	Sequence 743, App	954	112	3.6	990	2	US-08-479-722B-2	Sequence 2, Appli
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883	114	3.6	631	2	US-09-470-767-44123	Sequence 44123, A	956	112	3.6	1833	2	US-09-592-683-2	Sequence 2, Appli
884	114	3.6	644	1	US-08-866-757-2	Sequence 2, Appli	957	112	3.6	1833	4	US-09-592-683-2	Sequence 2, Appli
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889	114	3.6	1063	1	US-08-127-499A-8	Sequence 8, Appli	962	111.5	3.6	417	2	US-09-949-016-11097	Sequence 11097, A
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1019	110.5	3.5	675	2	US-09-332-063-3	Sequence 3, App1	1092	109	3.5	447	2	US-09-949-002-540	Sequence 540, App
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1023	110.5	3.5	1207	2	US-09-949-002-376	Sequence 376, App	1096	109	3.5	507	2	US-10-078-547-24	Sequence 24, App1
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1033	110.5	3.5	3724	1	US-09-105-537-6	Sequence 6, App1	1106	109	3.5	833	1	US-08-465-500-6	Sequence 6, App1
1034	110.5	3.5	3724	1	US-09-858-664A-11	Sequence 11, App1	1107	109	3.5	833	1	US-08-346-126-6	Sequence 6, App1
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1133	108.5	3.5	74	2	US-09-270-767-47979	Sequence 47979, A	1206	107.5	3.4	723	2	US-09-641-612-6	Sequence 6, Appl1
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1136	108.5	3.5	381	2	US-09-510-031A-5	Sequence 5, Appl1	1209	107.5	3.4	832	2	US-09-908-322-6	Sequence 6, Appl1
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1138	108.5	3.5	514	2	US-09-712-363-154	Sequence 154, App	1211	107.5	3.4	988	2	US-09-949-016-6695	Sequence 6695, Ap
1139	108.5	3.5	542	2	US-09-252-991A-21862	Sequence 21862, A	1212	107.5	3.4	1001	2	US-10-415-147-3	Sequence 3, Appl1
1140	108.5	3.5	548	1	US-08-468-576B-19	Sequence 19, Appl	1213	107.5	3.4	1088	2	US-09-233-857-13	Sequence 13, Appl
1141	108.5	3.5	548	1	US-08-468-576B-19	Sequence 19, Appl	1214	107.5	3.4	1135	1	US-08-574-959A-7	Sequence 7, Appl1
1142	108.5	3.5	548	2	US-08-468-576B-19	Sequence 19, Appl	1215	107.5	3.4	1135	2	US-09-357-014-7	Sequence 7, Appl1
1143	108.5	3.5	702	2	US-09-068-740A-4	Sequence 4, Appl1	1216	107.5	3.4	1327	2	US-09-949-016-8412	Sequence 8412, Ap
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1145	108.5	3.5	723	2	US-09-423-753-27	Sequence 27, Appl	1218	107	3.4	232	2	US-09-149-476-623	Sequence 623, App
1146	108.5	3.5	825	1	US-07-912-952-2	Sequence 2, Appl1	1219	107	3.4	288	2	US-09-252-991A-27676	Sequence 27676, A
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1150	108.5	3.5	1125	2	US-09-513-783A-152	Sequence 152, App	1223	107	3.4	369	2	US-09-252-991A-29670	Sequence 29670, A
1151	108.5	3.5	1125	2	US-09-430-656-152	Sequence 152, App	1224	107	3.4	492	2	US-09-252-991A-23619	Sequence 23619, A
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1153	108.5	3.5	1184	2	US-09-266-225D-18	Sequence 18, App	1226	107	3.4	541	2	US-10-101-464A-913	Sequence 913, App
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1155	108.5	3.5	1610	2	US-09-513-783A-22	Sequence 22, Appl	1228	107	3.4	615	2	US-09-949-002-301	Sequence 301, App
1156	108.5	3.5	1610	2	US-09-430-656-22	Sequence 22, Appl	1229	107	3.4	759	2	US-09-252-991A-19071	Sequence 19071, A
1157	108.5	3.5	1610	2	US-10-100-957A-22	Sequence 22, Appl	1230	107	3.4	793	2	US-09-252-991A-29395	Sequence 29395, A
1158	108	3.4	51	2	US-09-364-956-66	Sequence 66, Appl	1231	107	3.4	806	2	US-09-588-256-10	Sequence 10, Appl
1159	108	3.4	51	2	US-10-037-417-100	Sequence 10, App	1232	107	3.4	806	2	US-08-945-983-2	Sequence 2, Appl1
1160	108	3.4	152	2	US-09-214-909-22	Sequence 22, Appl	1233	107	3.4	1241	2	US-08-714-741-34	Sequence 34, Appl
1161	108	3.4	180	2	US-09-133-341-12	Sequence 12, Appl	1234	107	3.4	1315	2	US-08-899-595-3	Sequence 3, Appl1
1162	108	3.4	180	2	US-09-739-852-12	Sequence 12, Appl	1235	106.5	3.4	157	2	US-08-981-322-68	Sequence 68, Appl
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1164	108	3.4	590	1	US-08-785-310A-5	Sequence 5, Appl1	1237	106.5	3.4	157	2	US-09-310-685-20	Sequence 20, Appl
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1166	108	3.4	670	2	US-09-252-991A-32445	Sequence 32445, A	1239	106.5	3.4	176	2	US-09-270-767-47798	Sequence 47798, A
1167	108	3.4	703	2	US-09-367-206-5	Sequence 5, Appl1	1240	106.5	3.4	247	2	US-09-252-991A-23672	Sequence 23672, A
1168	108	3.4	703	2	US-09-298-404-5	Sequence 5, Appl1	1241	106.5	3.4	401	2	US-09-248-796A-26759	Sequence 26759, A
1169	108	3.4	705	2	US-09-902-540-11260	Sequence 11260, A	1242	106.5	3.4	420	2	US-09-902-540-13993	Sequence 13993, A
1170	108	3.4	820	2	US-09-252-991A-23346	Sequence 23346, A	1243	106.5	3.4	423	2	US-08-702-665A-5	Sequence 5, Appl1
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1172	108	3.4	1015	2	US-09-113-825-1	Sequence 1, Appl1	1245	106.5	3.4	464	2	US-09-366-009-7	Sequence 7, Appl1
1173	108	3.4	1189	2	US-09-287-354-3	Sequence 3, Appl1	1246	106.5	3.4	464	2	US-08-809-156B-7	Sequence 7, Appl1
1174	108	3.4	1320	2	US-10-164-595-58	Sequence 58, Appl	1247	106.5	3.4	464	2	US-09-775-964-7	Sequence 7, Appl1
1175	108	3.4	1404	2	US-10-164-595-78	Sequence 78, Appl	1248	106.5	3.4	489	2	US-09-366-009-8	Sequence 8, Appl1
1176	108	3.4	1411	2	US-09-949-016-10827	Sequence 10827, A	1249	106.5	3.4	489	2	US-08-809-156B-8	Sequence 8, Appl1
1177	108	3.4	1618	1	US-08-462-467B-4	Sequence 4, Appl1	1250	106.5	3.4	489	2	US-09-775-964-8	Sequence 8, Appl1
1178	108	3.4	1711	1	US-08-342-930-2	Sequence 2, Appl1	1251	106.5	3.4	575	2	US-08-923-865-2	Sequence 2, Appl1
1179	108	3.4	2887	2	US-08-462-467B-2	Sequence 2, Appl1	1252	106.5	3.4	575	2	US-09-510-949-2	Sequence 2, Appl1
1180	108	3.4	4551	2	US-09-320-878-1	Sequence 1, Appl1	1253	106.5	3.4	642	2	US-08-872-855-10	Sequence 10, Appl
1181	108	3.4	4551	2	US-09-141-908-2	Sequence 2, Appl1	1254	106.5	3.4	974	2	US-10-101-464A-921	Sequence 921, App
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1183	108	3.4	4551	2	US-09-793-708-1	Sequence 1, Appl1	1256	106.5	3.4	1003	1	US-08-909-984A-4	Sequence 4, Appl1
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1186	107.5	3.4	134	2	US-09-540-245A-12	Sequence 12, Appl	1259	106.5	3.4	1185	2	US-09-041-886-23	Sequence 23, Appl
1187	107.5	3.4	134	2	US-09-540-153-12	Sequence 12, Appl	1260	106.5	3.4	1185	2	US-09-538-092-1209	Sequence 1209, Ap
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1194	107.5	3.4	459	2	US-08-470-335-239	Sequence 239, App	1267	106.5	3.4	3594	2	US-09-911-842A-4	Sequence 4, Appl1
1195	107.5	3.4	459	2	US-08-467-602-299	Sequence 299, App	1268	106	3.4	115	2	US-09-621-976-4266	Sequence 4266, Ap

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1274	106	3.4	448	2	US-09-949-016-10130	Sequence 10130, A	1347	106	3.4	1244	2	US-09-386-123-46	Sequence 46, Appl
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1276	106	3.4	531	2	US-10-104-047-2775	Sequence 2775, Ap	1349	106	3.4	1244	2	US-10-007-747-46	Sequence 46, Appl
1277	106	3.4	666	2	US-09-050-739-70	Sequence 70, Appl	1350	106	3.4	1244	2	US-09-945-901-46	Sequence 46, Appl
1278	106	3.4	732	2	US-09-134-000C-6359	Sequence 6359, Ap	1351	106	3.4	1958	1	US-07-945-283-2	Sequence 2, Appl
1279	106	3.4	762	1	US-08-642-255-120	Sequence 120, App	1352	106	3.4	2185	2	US-09-854-856-36	Sequence 36, Appl
1280	106	3.4	762	1	US-08-397-633A-31	Sequence 31, Appl	1353	106	3.4	2185	2	US-10-010-720-36	Sequence 36, Appl
1281	106	3.4	763	2	US-09-949-016-10382	Sequence 10382, A	1354	106	3.4	2245	2	US-09-854-856-4	Sequence 4, Appl
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1283	106	3.4	1209	2	US-09-949-002-493	Sequence 493, App	1356	106	3.4	2322	2	US-09-854-856-34	Sequence 34, Appl
1284	106	3.4	1209	2	US-09-949-002-494	Sequence 494, App	1357	106	3.4	2322	2	US-10-010-720-34	Sequence 34, Appl
1285	106	3.4	1214	1	US-08-231-193A-54	Sequence 54, Appl	1358	106	3.4	2382	2	US-09-854-856-2	Sequence 2, Appl
1286	106	3.4	1214	1	US-08-486-273A-54	Sequence 54, Appl	1359	106	3.4	2382	2	US-10-010-720-2	Sequence 2, Appl
1287	106	3.4	1214	2	US-08-480-474-54	Sequence 54, Appl	1360	106	3.4	2743	2	US-10-037-182-36	Sequence 36, Appl
1288	106	3.4	1214	2	US-08-940-086A-54	Sequence 54, Appl	1361	106	3.4	2647	2	US-09-949-016-10932	Sequence 10932, A
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1291	106	3.4	1214	2	US-09-648-797-54	Sequence 54, Appl	1364	105.5	3.4	457	2	US-09-252-991A-17405	Sequence 17405, A
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1293	106	3.4	1214	2	US-10-038-937-54	Sequence 54, Appl	1366	105.5	3.4	486	2	US-09-538-092-1269	Sequence 1269, Ap
1294	106	3.4	1214	2	US-10-007-747-54	Sequence 54, Appl	1367	105.5	3.4	486	2	US-09-949-016-6151	Sequence 6151, Ap
1295	106	3.4	1219	2	US-09-945-901-54	Sequence 54, Appl	1368	105.5	3.4	510	2	US-08-246-489-2	Sequence 2, Appl
1296	106	3.4	1219	1	US-08-231-193A-50	Sequence 50, Appl	1369	105.5	3.4	559	2	US-10-116-370-2	Sequence 2, Appl
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1301	106	3.4	1219	2	US-08-935-105A-50	Sequence 50, Appl	1374	105.5	3.4	695	2	US-09-949-016-6102	Sequence 6102, Ap
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1314	106	3.4	1231	2	US-10-038-937-48	Sequence 48, Appl	1387	105.5	3.4	396	2	US-09-908-322-35	Sequence 35, Appl
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1331	106	3.4	1239	2	US-08-480-474-52	Sequence 52, Appl	1404	105	3.3	833	2	US-09-310-685-2	Sequence 2, Appl
1332	106	3.4	1239	2	US-08-940-086A-52	Sequence 52, Appl	1405	105	3.3	847	2	US-09-949-016-6222	Sequence 6222, Ap
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Db 241 SHVTLASPEETCHPPKAGRLLELDYADGCPATTTTAVTPRPVREPTALSSSL 300
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QY 541 GPGAGPLELEGVKKVPLEPGPKATEGGGEALPGSGSCEVPLMGFPGLQSPHAKPYI 598
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RESULT 2

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; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. 6734288ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. 6734288ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 69
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-457-69

Query Match 100.0%; Score 3135; DB 2; Length 598;
Best Local Similarity 100.0%; Pred. No. 6.6e-217;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCSRVPLLLPLLLLLALGPGVQCGSPGCGCQSQPOTVFTARQGTTPRDRVDPDTVGLVVF 60
Db 1 MCSRVPLLLPLLLLLALGPGVQCGSPGCGCQSQPOTVFTARQGTTPRDRVDPDTVGLVVF 60
QY 61 ENGITMLDASSFAGLPGQLLDLSQNIQIASRLPRLLLLDLSHNSLLALEPGILDANVE 120
Db 61 ENGITMLDASSFAGLPGQLLDLSQNIQIASRLPRLLLLDLSHNSLLALEPGILDANVE 120
QY 121 ALRLAGLQQLDGLFSRLNLHDLVDSDNQLRVPVIRGLRLTRILRAGNTRIAQL 180

Db 121 ALRLAGLQQLDEGLFSRLRNHLDVSDNQLRVPVIRGURGLTRLRAGNTRIAQL 180
Qy 181 RPEDLAGLAALQELDVSNLSLQALPGDLSGLFRLRLAAARNPFCVCPLSWFGPWVRE 240
Db 181 RPEDLAGLAALQELDVSNLSLQALPGDLSGLFRLRLAAARNPFCVCPLSWFGPWVRE 240
Qy 241 SHVTLASPBETRCHFPFKNAGRLLLBLDYADFQCPATTTATVPTTRPVVREPTALSSSL 300
Db 241 SHVTLASPBETRCHFPFKNAGRLLLBLDYADFQCPATTTATVPTTRPVVREPTALSSSL 300
Qy 301 APTWLSPTAPATAPSPSTAPTPGVPOQPCPSTCLNGTCHLGRHHLACLCPG 360
Db 301 APTWLSPTAPATAPSPSTAPTPGVPOQPCPSTCLNGTCHLGRHHLACLCPG 360
Qy 361 FTGLYCESOMGQGTSPPTVTPRPRSLTLGIEPVPSLSRLVQLQRYLQSSVQLRSRLR 420
Db 361 FTGLYCESOMGQGTSPPTVTPRPRSLTLGIEPVPSLSRLVQLQRYLQSSVQLRSRLR 420
Qy 421 LTYRNLGSPDKRLVTLRLPASLAEBYTVTQLRPNATYSVCVMPGLGKRVPEGEACGEAHT 480
Db 421 LTYRNLGSPDKRLVTLRLPASLAEBYTVTQLRPNATYSVCVMPGLGKRVPEGEACGEAHT 480
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Db 481 PPAVHSHAPVTVQAREGNLPLLIAPALAAVLAALAAVGAAYCVRGRAMAAAQDKGV 540
Qy 541 GPGAGPLEGKRVKVPLEPGPKATGEGGALPGSGCEVPLMGPPGGLQSPHLHAKPYI 598
Db 541 GPGAGPLEGKRVKVPLEPGPKATGEGGALPGSGCEVPLMGPPGGLQSPHLHAKPYI 598

RESULT 3

US-09-945-584-69
; Sequence 69, Application US/099455584
; Patent No. 6908993
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US/09/945,584
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694

; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/1146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. 6908993ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. 6908993ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 69
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-945-584-69

Query Match 100.0%; Score 3135; DB 2; Length 598;
Best Local Similarity 100.0%; Pred. No. 6.6e-217;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MCSRVPLLLPLLLALLGFGVGGCGCCSQPQVFCRTAROGTTVPRDVPDVTGLVVF 60
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Db 61 ENGITWLDASSFAGLPGQLLDLSQNIASLRLPRLLLDLSHNSLLALEPGILPTANVE 120
QY 121 ALRLAGLGLQDDEGLFSLRLNHLDVDNQLERVPPVIRGLRGLTRLRLAGNTRIAQL 180
Db 121 ALRLAGLGLQDDEGLFSLRLNHLDVDNQLERVPPVIRGLRGLTRLRLAGNTRIAQL 180
QY 181 REDLAGLAALQELDVSNLSLQALPGDLGSLFRLRLAAANPNPNCVCLPFWGPPWRE 240
Db 181 REDLAGLAALQELDVSNLSLQALPGDLGSLFRLRLAAANPNPNCVCLPFWGPPWRE 240
QY 241 SHVTLASPEBTRCHFPKKNAGRLLELDYADFPCPATTTTATVPTTRPVVREPTALSSSL 300
Db 241 SHVTLASPEBTRCHFPKKNAGRLLELDYADFPCPATTTTATVPTTRPVVREPTALSSSL 300
QY 301 APTWLSPTAPATEARSPSTAPTTPGVPPQDQCPSTCLNGTCHLGRHHLACLCPGEG 360
Db 301 APTWLSPTAPATEARSPSTAPTTPGVPPQDQCPSTCLNGTCHLGRHHLACLCPGEG 360
QY 361 FTGLYCESQMGOTRPSPTPTVPRPSLTGLIEPVSPSLRVGLQRYLQSSSVQLRSUR 420
Db 361 FTGLYCESQMGOTRPSPTPTVPRPSLTGLIEPVSPSLRVGLQRYLQSSSVQLRSUR 420
QY 421 LTYRNLGDPKRLVTLRLPASLAETVTQLRNATYSVCVMPGLGPRVPEGEACGEAHT 480
Db 421 LTYRNLGDPKRLVTLRLPASLAETVTQLRNATYSVCVMPGLGPRVPEGEACGEAHT 480
QY 481 PPAVHSHNAPVTOAREGNLPLLIAPALAAVLLAAVGAAYCVRGRGRAMAAADQKGV 540
Db 481 PPAVHSHNAPVTOAREGNLPLLIAPALAAVLLAAVGAAYCVRGRGRAMAAADQKGV 540
QY 541 GPGAGPLELEGVKVPLEPGPKATGEGGALPGSSCEVPLMGFPGQLQSPHLAKPYI 598
Db 541 GPGAGPLELEGVKVPLEPGPKATGEGGALPGSSCEVPLMGFPGQLQSPHLAKPYI 598

RESULT 4

US-09-944-944-69
; Sequence 69, Application US/09944944
; Patent No. 6929947
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tuma, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,944
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335

; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
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; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/216,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. 6929947ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. 6929947ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 69
; LENGTH: 598
; TYPE: PRT

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; ORGANISM: Homo Sapien
; US-09-944-944-69

Query Match      100.0%; Score 3135; DB 2; Length 598;
Best Local Similarity 100.0%; Pred. No. 6.6e-217;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCSRVPLLLPLLLLLALGPGVQCPCGCGCQSQQTVCFTARQQTTPRDPVPPDTGLVYF 60
DB 1 MCSRVPLLLPLLLLLALGPGVQCPCGCGCQSQQTVCFTARQQTTPRDPVPPDTGLVYF 60

QY 61 ENGITWLDASSFAGLQGLQDLDSQOIASLRLPRLLLDLSHNSLLALEPGLDTPANVE 120
DB 61 ENGITWLDASSFAGLQGLQDLDSQOIASLRLPRLLLDLSHNSLLALEPGLDTPANVE 120

QY 121 ALRLAGLGLQQLDEGLFSRLNLHDLVDSDNQLRVPVIRGLRGLTRLRLAGNTRIAQL 180
DB 121 ALRLAGLGLQQLDEGLFSRLNLHDLVDSDNQLRVPVIRGLRGLTRLRLAGNTRIAQL 180

QY 181 RPEDLAGLAALQELDVSNLSLQALPGDLGSLFRLRLAAARNPFCVPLSWFGPWVRE 240
DB 181 RPEDLAGLAALQELDVSNLSLQALPGDLGSLFRLRLAAARNPFCVPLSWFGPWVRE 240

QY 241 SHVTLASPETRCHFPFKNAGRLILLDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300
DB 241 SHVTLASPETRCHFPFKNAGRLILLDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300

QY 301 APTWLSPTAPATEAPSPPTAPTPVGPVPOPCPPSTCLNGTCHLGRHHLACI-CPEG 360
DB 301 APTWLSPTAPATEAPSPPTAPTPVGPVPOPCPPSTCLNGTCHLGRHHLACI-CPEG 360

QY 361 FTGLYCESQMGQGTSPSTPTVTPRPRSLTLGIEPVSPSTSLRVLQRYLQGSVVQLRSRL 420
DB 361 FTGLYCESQMGQGTSPSTPTVTPRPRSLTLGIEPVSPSTSLRVLQRYLQGSVVQLRSRL 420

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QY 481 PPAVSHNAPVTQAREGNPLLIAPALAAVLAALAAVCAAYCVRGRGRAMAAADKGV 540
DB 481 PPAVSHNAPVTQAREGNPLLIAPALAAVLAALAAVCAAYCVRGRGRAMAAADKGV 540

QY 541 GPGAGPLEGKVKVPLEPGPKATEGGGEALPSSGECEVPLMGFPGLQSPHLHAKPYI 598
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RESULT 5
US-09-945-587-69
; Sequence 69, Application US/09945587
; Patent No. 6936254
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/945,587
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: November 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: November 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/25108
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
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; PRIOR FILING DATE: September 15, 1999
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; PRIOR FILING DATE: No. 6936254ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. 6936254ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
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; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
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; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 69
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-945-587-69

Query Match 100.0%; Score 3135; DB 2; Length 598;
Best Local Similarity 100.0%; Pred. No. 6 6e-217;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCSRVPLLLPLLLLALGPGVQGCPSGCQSQPQTARQGTTPRDRVPPDTVGLYVF 60
Db 1 MCSRVPLLLPLLLLALGPGVQGCPSGCQSQPQTARQGTTPRDRVPPDTVGLYVF 60

QY 61 ENGITMDASSFAGLPGQLLDLSQNIASLRLPRLLLDLSHNSLLALEPGILTANVE 120
Db 61 ENGITMDASSFAGLPGQLLDLSQNIASLRLPRLLLDLSHNSLLALEPGILTANVE 120

QY 121 ALRLAGLGLQOQDEGLFSLRLNLDVSDNQLERVPVIRGLGLTRLRLAGNTRIAQL 180
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Db 181 RPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLAAAARNPNCVPLSWFGPWVRE 240

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Db 241 SHVTLASPBETRCHFPKKNAGRLLELDYADFGCPATTTATVTPTRPVREPTALSSSL 300

QY 301 APTWLSPTAPATEAPSPSTAPPTVGPVPODPCPSTCLNGTCHLGRHHLACLCPBG 360
Db 301 APTWLSPTAPATEAPSPSTAPPTVGPVPODPCPSTCLNGTCHLGRHHLACLCPBG 360

QY 361 FTGLYCESQMGQGTSPSTPTVTPRPRSLTLGIEPVSTLSRVGLQRYLQGSVVQLRSRL 420
Db 361 FTGLYCESQMGQGTSPSTPTVTPRPRSLTLGIEPVSTLSRVGLQRYLQGSVVQLRSRL 420

QY 421 LTYRNLSGDKRLVTLRLPASLAETVTLRPNATYSVCVMPLEGRVPEGEACGEAHT 480
Db 421 LTYRNLSGDKRLVTLRLPASLAETVTLRPNATYSVCVMPLEGRVPEGEACGEAHT 480

QY 481 PPAVHSHNAPVTOAREGNLPLLIAPALAAVLLAAVGAAYCVRGRAMAAADKGOV 540
Db 481 PPAVHSHNAPVTOAREGNLPLLIAPALAAVLLAAVGAAYCVRGRAMAAADKGOV 540

QY 541 GPGAGPLEGKVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGLQSPHAKPYI 598
Db 541 GPGAGPLEGKVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGLQSPHAKPYI 598

RESULT 6
US-09-063-950-2
; Sequence 2, Application US/09063950C
; Patent No. 6225085
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL LRSG PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; FILE OF INVENTION: THEREFOR
; FILE REFERENCE: MEI-019
; CURRENT APPLICATION NUMBER: US/09/063,950C
; CURRENT FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-063-950-2

Query Match 98.4%; Score 3083.5; DB 2; Length 673;
Best Local Similarity 88.7%; Pred. No. 3.8e-213;
Matches 597; Conservative 0; Mismatches 1; Indels 75; Gaps 1;

QY 1 MCSRVPLLLPLLLLALGPGVQGCPSGCQSQPQTARQGTTPRDRVPPDTVGLYVF 60
Db 1 MCSRVPLLLPLLLLALGPGVQGCPSGCQSQPQTARQGTTPRDRVPPDTVGLYVF 60

QY 61 ENGITMDASSFAGLPGQLLDLSQNIASLRLPRLLLDLSHNS 105
Db 61 ENGITMDASSFAGLPGQLLDLSQNIASLRLPRLLLDLSHNS 105

QY 91 -----LRLPRLLLDLSHNS 105
Db 91 -----LRLPRLLLDLSHNS 105

QY 121 RGLRLRLRYLGNKRIHQPCAFDTLDRLLLELKLQDNELRALPRLRLPRLLLDLSHNS 180
Db 121 RGLRLRLRYLGNKRIHQPCAFDTLDRLLLELKLQDNELRALPRLRLPRLLLDLSHNS 180

QY 106 LLALPEGLDITANVEALRLAGLGLQOQDEGLFSLRLNLDVSDNQLERVPVIRGLRG 165
Db 106 LLALPEGLDITANVEALRLAGLGLQOQDEGLFSLRLNLDVSDNQLERVPVIRGLRG 165

QY 181 LLALPEGLDITANVEALRLAGLGLQOQDEGLFSLRLNLDVSDNQLERVPVIRGLRG 240
Db 181 LLALPEGLDITANVEALRLAGLGLQOQDEGLFSLRLNLDVSDNQLERVPVIRGLRG 240

QY 166 LTRRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLAAAARNPF 225
Db 166 LTRRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLAAAARNPF 225

QY 241 LTRRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLAAAARNPF 300
Db 241 LTRRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLAAAARNPF 300

QY 226 NCVCLPSWFGPWVRESHVTLASPBETRCHFPKKNAGRLLELDYADFGCPATTTATVPT 285
Db 226 NCVCLPSWFGPWVRESHVTLASPBETRCHFPKKNAGRLLELDYADFGCPATTTATVPT 285

QY 301 NCVCLPSWFGPWVRESHVTLASPBETRCHFPKKNAGRLLELDYADFGCPATTTATVPT 360
Db 301 NCVCLPSWFGPWVRESHVTLASPBETRCHFPKKNAGRLLELDYADFGCPATTTATVPT 360

QY 286 TRPVVREPTALSSSLAPTWLSPTAPATEAPSPSTAPPTVGPVPODPCPSTCLNGGTC 345
Db 286 TRPVVREPTALSSSLAPTWLSPTAPATEAPSPSTAPPTVGPVPODPCPSTCLNGGTC 345

QY 361 TRPVVREPTALSSSLAPTWLSPTAPATEAPSPSTAPPTVGPVPODPCPSTCLNGGTC 420
Db 361 TRPVVREPTALSSSLAPTWLSPTAPATEAPSPSTAPPTVGPVPODPCPSTCLNGGTC 420

QY 346 HLGRHHLACLCPBGFTGLYCESQMGQGTSPSTPTVTPRPRSLTLGIEPVSTLSRVGL 405
Db 346 HLGRHHLACLCPBGFTGLYCESQMGQGTSPSTPTVTPRPRSLTLGIEPVSTLSRVGL 405

QY 421 HLGRHHLACLCPBGFTGLYCESQMGQGTSPSTPTVTPRPRSLTLGIEPVSTLSRVGL 480
Db 421 HLGRHHLACLCPBGFTGLYCESQMGQGTSPSTPTVTPRPRSLTLGIEPVSTLSRVGL 480

QY 406 QRYLQGSVVQLRSRLTYRNLSGDKRLVTLRLPASLAETVTLRPNATYSVCVMPLEGP 465
Db 406 QRYLQGSVVQLRSRLTYRNLSGDKRLVTLRLPASLAETVTLRPNATYSVCVMPLEGP 465

QY 481 QRYLQGSVVQLRSRLTYRNLSGDKRLVTLRLPASLAETVTLRPNATYSVCVMPLEGP 540
Db 481 QRYLQGSVVQLRSRLTYRNLSGDKRLVTLRLPASLAETVTLRPNATYSVCVMPLEGP 540

QY 466 GRVPEGEACGEAHTPPAVHSHNAPVTOAREGNLPLLIAPALAAVLLAAVGAAYCVR 525
Db 466 GRVPEGEACGEAHTPPAVHSHNAPVTOAREGNLPLLIAPALAAVLLAAVGAAYCVR 525

QY 541 GRVPEGEACGEAHTPPAVHSHNAPVTOAREGNLPLLIAPALAAVLLAAVGAAYCVR 600
Db 541 GRVPEGEACGEAHTPPAVHSHNAPVTOAREGNLPLLIAPALAAVLLAAVGAAYCVR 600

QY 526 RGRAMAAADKGOVQGVGAGPLEGKVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPFG 585
Db 526 RGRAMAAADKGOVQGVGAGPLEGKVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPFG 585

QY 601 RGRAMAAADKGOVQGVGAGPLEGKVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPFG 660
Db 601 RGRAMAAADKGOVQGVGAGPLEGKVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPFG 660

QY 586 PGLQSPHAKPYI 598
Db 586 PGLQSPHAKPYI 598

QY 661 PGLQSPHAKPYI 673
Db 661 PGLQSPHAKPYI 673

RESULT 7
US-09-991-181-52
; Sequence 52, Application US/09991181
; Patent No. 6913919
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C53
CURRENT APPLICATION NUMBER: US/09/991,181
CURRENT FILING DATE: 2001-11-16
PRIORITY APPLICATION NUMBER: 60/049787
PRIORITY FILING DATE: 1997-06-16
PRIORITY APPLICATION NUMBER: 60/062250
PRIORITY FILING DATE: 1997-10-17
PRIORITY APPLICATION NUMBER: 60/065186
PRIORITY FILING DATE: 1997-11-12
PRIORITY APPLICATION NUMBER: 60/065311
PRIORITY FILING DATE: 1997-11-13
PRIORITY APPLICATION NUMBER: 60/066770
PRIORITY FILING DATE: 1997-11-24
PRIORITY APPLICATION NUMBER: 60/075945
PRIORITY FILING DATE: 1998-02-25
PRIORITY APPLICATION NUMBER: 60/078910
PRIORITY FILING DATE: 1998-03-20
PRIORITY APPLICATION NUMBER: 60/083322
PRIORITY FILING DATE: 1998-04-28
PRIORITY APPLICATION NUMBER: 60/084600
PRIORITY FILING DATE: 1998-05-07
PRIORITY APPLICATION NUMBER: 60/087106
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PRIORITY FILING DATE: 1998-06-18
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PRIORITY APPLICATION NUMBER: 60/090444
PRIORITY FILING DATE: 1998-06-24
PRIORITY APPLICATION NUMBER: 60/090445
PRIORITY FILING DATE: 1998-06-24
PRIORITY APPLICATION NUMBER: 60/090472
PRIORITY FILING DATE: 1998-06-24
PRIORITY APPLICATION NUMBER: 60/090535
PRIORITY FILING DATE: 1998-06-24
PRIORITY APPLICATION NUMBER: 60/090540
PRIORITY FILING DATE: 1998-06-24

		Query Match		↓	98.4%;	Score 3083.5;	DB 2;	Length 673;
		Best Local Similarity			88.7%;	Pred. No. 3.8e-213;		
		Matches 597;		Conservative	0;	Mismatches	1;	Gaps 1;
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	1	MCSRVP	LLP	LLP	LLP	LLP	LLP	LLP
Db	1	MCSRVP	LLP	LLP	LLP	LLP	LLP	LLP
	1	MCSRVP	LLP	LLP	LLP	LLP	LLP	LLP
QY	61	ENGIT	MD	ASS	PAG	LP	GL	LD
	61	ENGIT	MD	ASS	PAG	LP	GL	LD
Db	91	-----	-----	-----	-----	-----	-----	-----
	91	-----	-----	-----	-----	-----	-----	-----
QY	121	RGLR	LER	LY	LGN	RI	HP	CA
	121	RGLR	LER	LY	LGN	RI	HP	CA
Db	106	LAL	EP	GL	DT	AN	VA	LR
	181	LAL	EP	GL	DT	AN	VA	LR
QY	166	LTR	LAG	N	TR	IA	Q	RP
	241	LTR	LAG	N	TR	IA	Q	RP
Db	226	NCV	PL	S	FW	GP	W	R
	301	NCV	PL	S	FW	GP	W	R
QY	286	TPV	VR	EP	T	AL	S	S
	361	TPV	VR	EP	T	AL	S	S
Db	346	HLG	TR	H	L	A	C	L
	346	HLG	TR	H	L	A	C	L

102 PRIOR APPLICATION NUMBER: 60/090542

103 PRIOR FILING DATE: 1998-06-24

104 PRIOR APPLICATION NUMBER: 60/090557

105 PRIOR FILING DATE: 1998-06-24

106 PRIOR APPLICATION NUMBER: 60/090676

107 PRIOR FILING DATE: 1998-06-25

108 PRIOR APPLICATION NUMBER: 60/090678

109 PRIOR FILING DATE: 1998-06-25

110 PRIOR APPLICATION NUMBER: 60/090690

111 PRIOR FILING DATE: 1998-06-25

112 PRIOR APPLICATION NUMBER: 60/090694

113 PRIOR FILING DATE: 1998-06-25

114 PRIOR APPLICATION NUMBER: 60/090695

115 PRIOR FILING DATE: 1998-06-25

116 PRIOR APPLICATION NUMBER: 60/090696

117 PRIOR FILING DATE: 1998-06-25

118 PRIOR APPLICATION NUMBER: 60/090862

119 PRIOR FILING DATE: 1998-06-26

120 PRIOR APPLICATION NUMBER: 60/090863

121 PRIOR FILING DATE: 1998-06-26

122 PRIOR APPLICATION NUMBER: 60/091360

123 PRIOR FILING DATE: 1998-07-01

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125 PRIOR FILING DATE: 1998-07-02

126 PRIOR APPLICATION NUMBER: 60/091544

127 PRIOR FILING DATE: 1998-07-01

128 PRIOR APPLICATION NUMBER: 60/091519

129 PRIOR FILING DATE: 1998-07-02

130 PRIOR APPLICATION NUMBER: 60/091626

131 PRIOR FILING DATE: 1998-07-02

132 PRIOR APPLICATION NUMBER: 60/091633

133 PRIOR FILING DATE: 1998-07-02

134 PRIOR APPLICATION NUMBER: 60/091978

135 PRIOR FILING DATE: 1998-07-07

136 PRIOR APPLICATION NUMBER: 60/091982

137 PRIOR FILING DATE: 1998-07-07

138 PRIOR APPLICATION NUMBER: 60/092182

139 PRIOR FILING DATE: 1998-07-09

421 HLGTRHLLACLCPEGFTGLYCESOMQGTSPPTVTPRPRSLTLGIEPVSPSPTSLRVGL 480

406 QRYLOGSSVOLRSRLTYRNLSGPDKRLVTLRLPASLAETVTLRPNATYSVCVMPGLP 465

481 QRYLOGSSVOLRSRLTYRNLSGPDKRLVTLRLPASLAETVTLRPNATYSVCVMPGLP 540

466 GRVPEGEACGEAHTPPAVHNSHAPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVR 525

541 GRVPEGEACGEAHTPPAVHNSHAPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVR 600

526 RGRAMAAAQDKGVGPGAGPLEGKVPLEPGKATEGGSEALPSGSECEVPLMGPPG 585

601 RGRAMAAAQDKGVGPGAGPLEGKVPLEPGKATEGGSEALPSGSECEVPLMGPPG 660

586 PGLQSLHAKPYI 598

661 PGLQSLHAKPYI 673

RESULT 8

US-09-990-444-52

Sequence 52, Application US/09990444

Patent No. 6930170

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

FILE REFERENCE: P2730PIC19

CURRENT APPLICATION NUMBER: US/09/990,444

CURRENT FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945

PRIOR FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/083322

PRIOR FILING DATE: 1998-04-28

PRIOR APPLICATION NUMBER: 60/084600

PRIOR FILING DATE: 1998-05-07

PRIOR APPLICATION NUMBER: 60/087106

PRIOR FILING DATE: 1998-05-28

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64	PRIOR FILING DATE: 1998-06-17
65	PRIOR APPLICATION NUMBER: 60/089600
66	PRIOR FILING DATE: 1998-06-17
67	PRIOR APPLICATION NUMBER: 60/089653
68	PRIOR FILING DATE: 1998-06-17
69	PRIOR APPLICATION NUMBER: 60/089801

1	PRIOR FILING DATE: 1998-06-18
2	PRIOR APPLICATION NUMBER: 60/089907
3	PRIOR FILING DATE: 1998-06-18
4	PRIOR APPLICATION NUMBER: 60/089908
5	PRIOR FILING DATE: 1998-06-18
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22	PRIOR APPLICATION NUMBER: 60/090429
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67	PRIOR FILING DATE: 1998-07-02
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69	PRIOR FILING DATE: 1998-07-02
70	PRIOR APPLICATION NUMBER: 60/091978
71	PRIOR FILING DATE: 1998-07-07
72	PRIOR APPLICATION NUMBER: 60/091982
73	PRIOR FILING DATE: 1998-07-07

; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 98.4%; Score 3083.5; DB 2; Length 673;
Best Local Similarity 88.7%; Pred. No. 3.8e-213;
Matches 597; Conservative 0; Mismatches 1; Indels 75;

Qy	1	MCSRPVLLPLILLIALLGGVQCPCSGCCSQCPQTVCTARQGTTPVRDVPPTVGLYVF	60
Db	1	MCSRPVLLPLILLIALLGGVQCPCSGCCSQCPQTVCTARQGTTPVRDVPPTVGLYVF	60
Qy	61	ENGITWLDASSFAGLPGQLLDLSQNIAS-----	90
Db	61	ENGITWLDAGSFAGLPGQLLDLSQNIASLPSGVFQPLANLSNLDLTANRLHEITNETF	120
Qy	91	-----LRLPRLLLLLDLSHNS	105
Db	121	RGLRLRLRYLQKNRIRHIQCAFEDTLDRLLLEKLQDNELRALPURLPRLLLDLSHNS	180
Qy	106	LLALBPGILDTANVEALRLAGLGLQQLDEGLFSLRNLHDLVDSDQLERVPVIRGLG	165
Db	181	LLALBPGILDTANVEALRLAGLGLQQLDEGLFSLRNLHDLVDSDQLERVPVIRGLG	240
Qy	166	LTRLRLAGNTRIAQLRPSDLAGLAAQLBELDVSNLSLOALPGDLSGLFPRRLRLAAARNPF	225
Db	241	LTRLRLAGNTRIAQLRPSDLAGLAAQLBELDVSNLSLOALPGDLSGLFPRRLRLAAARNPF	300
Qy	226	NCVCPUSWFGPMWRSHVTLASPEPTRCHRPKKNAGRLLELDYADFQCPATTTTATVPT	285
Db	301	NCVCPUSWFGPMWRSHVTLASPEPTRCHFPKKNAGRLLELDYADFQCPATTTTATVPT	360
Qy	286	TRPVREPTALSSSLAPTWMLSPTAPATEAPSPSTAPTTPGVPPQDCPPSPCLNGGTC	345
Db	361	TRPVREPTALSSSLAPTWMLSPTAPATEAPSPSTAPTTPGVPPQDCPPSPCLNGGTC	420
Qy	346	HGTRHHLACLCEPFGTGLYCESQMGQTRSPTPTVPRPRSLTIGIEBVSFSTSLRVGL	405
Db	421	HGTRHHLACLCEPFGTGLYCESQMGQTRSPTPTVPRPRSLTIGIEBVSFSTSLRVGL	480
Qy	406	QRYLQSSSVQLRSLRLTYRNLSGDPDKRLVTURLPASLAEYTVTLQLRPNATYSVCVMPLGP	465
Db	481	QRYLQSSSVQLRSLRLTYRNLSGDPDKRLVTURLPASLAEYTVTLQLRPNATYSVCVMPLGP	540
Qy	466	GRVPEGEBAAGBAHTPPAVHNSHAPVTOAREGNIPLLIAPALAAVLALAAVGAAYCYVR	525
Db	541	GRVPEGEBAAGBAHTPPAVHNSHAPVTOAREGNIPLLIAPALAAVLALAAVGAAYCYVR	600
Qy	526	RGRMAAAAOQKGVGPGAGPLELEGVKVPLEPGPKATEGGGREALPSGSECEVPLMGFP	585
Db	601	RGRMAAAAOQKGVGPGAGPLELEGVKVPLEPGPKATEGGGREALPSGSECEVPLMGFP	660
Qy	586	PGQLQSPHLHAKPYI	598
Db	661	PGQLQSPHLHAKPYI	673

RESULT 9

US-09-997-333-52
; Sequence 52, Application US/09997333
; Patent No. 6953836

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
 ; Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Giodowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher


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; PRIOR APPLICATION NUMBER: 60/091982
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match          98.4%; Score 3083.5; DB 2; Length 673;
Best Local Similarity 88.7%; Pred. No. 3.8e-213;
Matches 597; Conservative 0; Mismatches 1; Indels 75; Gaps 1;

Qy 1 MCSRVPLLLPLLLLLALGFGVQCGPSCGCCSQPQTVFCTARQGTTPRDVPPDTVGLVVF 60
Db 1 MCSRVPLLLPLLLLLALGFGVQCGPSCGCCSQPQTVFCTARQGTTPRDVPPDTVGLVVF 60
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Db 61 ENGITMLDAGSFAGLPGLQLDLSONQIAS----- 90
Qy 91 -----LRLPRLLLLDLSHNS 105
Db 121 RGLRRLRLYLGNRIHQFGAFDTLDRLELKLQDNELRALPRLRLPLLLDLSHNS 180
Qy 106 LLALPEGLDTANVEALRLAGLQQLDEGLFSLRLNHLHDVSDNQLERVPVIRGLRG 165
Db 181 LLALPEGLDTANVEALRLAGLQQLDEGLFSLRLNHLHDVSDNQLERVPVIRGLRG 240
Qy 166 LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLISGLFRLRLAARNPF 225
Db 241 LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLISGLFRLRLAARNPF 300
Qy 226 NVCPLSWFGPWVRESHVTLASPEETRCHFPKKNAGRLLLLELDVADFCGPATTTATVPT 285
Db 301 NVCPLSWFGPWVRESHVTLASPEETRCHFPKKNAGRLLLLELDVADFCGPATTTATVPT 360
Qy 286 TRPVVREPTALSSSLAPTWSPTAPATEAPSPSTAPPTVGPVQPQDCPSTCLNGGTC 345
Db 361 TRPVVREPTALSSSLAPTWSPTAPATEAPSPSTAPPTVGPVQPQDCPSTCLNGGTC 420
Qy 346 HLGTRHHLACLCPGFTGLCYCESQMGQTRSPTRPFRPSRLTLGIEPVSPLSRVGL 405
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Db 481 QRYLOGSSVOLBSLRLTYRNLSPDKRLVTLRLPASLAEYVTVQLRPNATYSVCVMPGLP 540
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QY 526 RGRMAAAADQKQVGPAGPGLLEGVKVPFLPFGPKATEGGGEALPSGSECEVPLMGFPFG 585
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QY 586 PGLQSPHLHAKPYI 598
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RESULT 10
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; Sequence 52, Application US/09992598
; Patent No. 6956108
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napiej, Mary A.
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC20
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Query Match 98.4%; Score 3083.5; DB 2; Length 673;
Best Local Similarity 88.7%; Pred. No. 3.8e-213;
Matches 597; Conservative 0; Mismatches 1; Indels 75; Gaps 1;

QY 1 MCSRVPLLLPLLLLLALGPGVGCPCSGCOCSPQTVFCTARQCTTVPDRVPPDVTGLYVF 60
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DB 61 ENGITMLDAGSFAGLPGLQLDLDSQNOIASLPSGVFQPLANLSNLDLTANRLHEITNETF 120

QY 91 -----LRLPRLLLLDLSHNS 105
DB 121 RGLRLRLRYLGNRIHQGAFTDLRLLELKLQDNELRALPPRLPRLLLLDLSHNS 180

QY 106 LLALEPGILDANVEALRLAGLQQLDEGLFSRLNLHDLVDSDNQLERVPVIRGLRG 165
DB 181 LLALEPGILDANVEALRLAGLQQLDEGLFSRLNLHDLVDSDNQLERVPVIRGLRG 240

QY 166 LTRLRLAGNTRIAQLRPEDLAGLAALQELDVNSLSLQALPGDLGSLFPRLLRLAAARNPF 225
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QY 286 TRPVVREPTALSSSLAPTWSLPTAPATEAPSPSTAPPTVGPVPOQDCPPSTCLNGGTC 345
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QY 526 RGRAMAAAAQDKGVGPGAGPLELEGVKVPLEFPGPKATEGGGEALPSGSECEVPLMGFP 585
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DB 661 PGLQSPHLAKPYI 673

RESULT 11
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; Patent No. 6689866
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
; FILE REFERENCE: 15966-540 No. 6689866el Polynucleotides
; CURRENT APPLICATION NUMBER: US/09520,781
; CURRENT FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: USSN 60/123,667
; PRIOR FILING DATE: 1999-03-09
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 653

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; ORGANISM: Homo sapiens
US-09-520-781-10

Query Match      10.7%; Score 337; DB 2; Length 653;
Best Local Similarity 23.6%; Pred. No. 5.1e-16;
Matches 159; Conservative 77; Mismatches 231; Indels 206; Gaps 25;

QY 7 LLLPLLLL-----LALGPGVQCSPGCCS-QPQVCTARQGTTPRDVDPD 53
Db 17 ILLPFVYLTAQWILCAIAAASAGPQNCPSVCSCNQFSKVCTRRGLSEVPQIPSN 76
QY 54 TVGLVVFENGITMLDASSFAGLPGQLQLDLSONQIASLR-----LPRLLLDLSHNSIL 107
Db 77 TRYLMNMENNIQMIQADTFRHLHLEVLQLGKNSIRQIEVGAFAENGLASLSTLELFDNWL 136
QY 108 ALEPGILDAN-----VEALRLAGLG-----LQQLDEGLFSRLR 141
Db 137 VIPSGAFEYLSKRLWLNRNPIESIPYAFNRVPSLMRLDLGELKLEYISEGAFEGLF 196
QY 142 N-----LHLDVSDNQLERV-PPVIRGLRGLTRLRAGNTRIA 178
Db 197 NLKYLNLGMCNIKOMPNTPLVGLLEEMSGNHPEIRPGSFHGLSSLKLLWVM-NSQVS 255
QY 179 QLRPEDLAGLAALQELDVNSLSQALPGDLGLFPRLRLAAA---RNPFNCVCPLSWFG 235
Db 256 LIERNAFDGLASIVELNLAHNNLSLPHD---LFTPLRYLVELHLHHPNWCDCDILMLA 312
QY 236 PWRRESHVTLASPEETRCHFPKNAAGRLLELDYADFCGPATTTTATVTPTRPVVREPTA 295
Db 313 WMLRE-YIPTNSTCCGRCHAPMHRGRYLVVDQASFOCSA-----PFIMDAPRDLNI 364
QY 296 LSSSLAP-----TWLSPTAPA-TEAPSPSTAPPTVGPVPQP-----QDCPPSTC 339
Db 365 SEGRMAELKCRTPPMSSSVKMLLPNGTVLSHARHPRISVLNDGTLNFHSHVLLSDTGVTY 424
QY 340 -----LNGGTCHLGRHHLACLCPGFTGLYCESQMGQTRPSPTVTP-- 383
Db 425 MGTNVAGNSNASAYLNGSTAEINTSNY-----SFFTGTGETTEISPEDTTRKY 473
QY 384 RPPRSLTGLIEPVSPTSRVLGQRYLOGSSVQLRSLRSLTYRNLSPDKRLVTLRLPASLA 443
Db 474 KPVPITSTGYQPAYTTSTTVLIQ-----TTDKMOTSLDEVKMTTK-----II 529
QY 444 EYTVTLRPNATYSVCVMPGLGPRVPEGEACGEAHTPPAVHSNHPVTOAREGNLPLLI 503
Db 506 -----VPATD-----TTDKMOTSLDEVKMTTK-----II 529
QY 504 APALAAVLLAALAAVGAAYCYRR---GRAMAAAAQDKGVGPGAGPLEGKVKVLEPGP 560
Db 530 IGCFAVVTLLAAAMLIVFYKLRKHQRQSRSTVTAAR-----TVEIIQVD-EDIP 576
QY 561 KATEGGEGALPSG 573
Db 577 AATSAATAAPSG 589

RESULT 13
US-09-957-187-10
; Sequence 10, Application US/09991053
; Patent No. 6942992
; GENERAL INFORMATION:
; APPLICANT: Shimketa, Richard A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES ENCODING HUMAN SLIT-,
; FILE REFERENCE: 15966-540 CIP
; CURRENT APPLICATION NUMBER: US/09/957,187
; PRIORITY FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/234,082

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-520-781-10

Query Match      10.7%; Score 337; DB 2; Length 653;
Best Local Similarity 23.6%; Pred. No. 5.1e-16;
Matches 159; Conservative 77; Mismatches 231; Indels 206; Gaps 25;

QY 7 LLLPLLLL-----LALGPGVQCSPGCCS-QPQVCTARQGTTPRDVDPD 53
Db 17 ILLPFVYLTAQWILCAIAAASAGPQNCPSVCSCNQFSKVCTRRGLSEVPQIPSN 76
QY 54 TVGLVVFENGITMLDASSFAGLPGQLQLDLSONQIASLR-----LPRLLLDLSHNSIL 107
Db 77 TRYLMNMENNIQMIQADTFRHLHLEVLQLGKNSIRQIEVGAFAENGLASLSTLELFDNWL 136
QY 108 ALEPGILDAN-----VEALRLAGLG-----LQQLDEGLFSRLR 141
Db 137 VIPSGAFEYLSKRLWLNRNPIESIPYAFNRVPSLMRLDLGELKLEYISEGAFEGLF 196
QY 142 N-----LHLDVSDNQLERV-PPVIRGLRGLTRLRAGNTRIA 178
Db 197 NLKYLNLGMCNIKOMPNTPLVGLLEEMSGNHPEIRPGSFHGLSSLKLLWVM-NSQVS 255
QY 179 QLRPEDLAGLAALQELDVNSLSQALPGDLGLFPRLRLAAA---RNPFNCVCPLSWFG 235
Db 256 LIERNAFDGLASIVELNLAHNNLSLPHD---LFTPLRYLVELHLHHPNWCDCDILMLA 312
QY 236 PWRRESHVTLASPEETRCHFPKNAAGRLLELDYADFCGPATTTTATVTPTRPVVREPTA 295
Db 313 WMLRE-YIPTNSTCCGRCHAPMHRGRYLVVDQASFOCSA-----PFIMDAPRDLNI 364
QY 296 LSSSLAP-----TWLSPTAPA-TEAPSPSTAPPTVGPVPQP-----QDCPPSTC 339
Db 365 SEGRMAELKCRTPPMSSSVKMLLPNGTVLSHARHPRISVLNDGTLNFHSHVLLSDTGVTY 424
QY 340 -----LNGGTCHLGRHHLACLCPGFTGLYCESQMGQTRPSPTVTP-- 383
Db 425 MGTNVAGNSNASAYLNGSTAEINTSNY-----SFFTGTGETTEISPEDTTRKY 473
QY 384 RPPRSLTGLIEPVSPTSRVLGQRYLOGSSVQLRSLRSLTYRNLSPDKRLVTLRLPASLA 443
Db 474 KPVPITSTGYQPAYTTSTTVLIQ-----TTDKMOTSLDEVKMTTK-----II 529
QY 444 EYTVTLRPNATYSVCVMPGLGPRVPEGEACGEAHTPPAVHSNHPVTOAREGNLPLLI 503
Db 506 -----VPATD-----TTDKMOTSLDEVKMTTK-----II 529
QY 504 APALAAVLLAALAAVGAAYCYRR---GRAMAAAAQDKGVGPGAGPLEGKVKVLEPGP 560
Db 530 IGCFAVVTLLAAAMLIVFYKLRKHQRQSRSTVTAAR-----TVEIIQVD-EDIP 576
QY 561 KATEGGEGALPSG 573
Db 577 AATSAATAAPSG 589

RESULT 12
US-09-957-187-10
; Sequence 10, Application US/09957187
; Patent No. 6863889
; GENERAL INFORMATION:
; APPLICANT: Shimketa, Richard A.
; APPLICANT: LaRoche, William
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
; FILE REFERENCE: 15966-540 CIP
; CURRENT APPLICATION NUMBER: US/09/957,187
; PRIORITY FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/234,082
```

; TITLE OF INVENTION: MEGF-, AND ROUNDABOUT-LIKE POLYPEPTIDES
; FILE REFERENCE: 15966-540 CON S-10
; CURRENT APPLICATION NUMBER: US/09/991,053
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: USSN 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-991-053-10

Query Match 10.7%; Score 337; DB 2; Length 653;
Best Local Similarity 23.6%; Pred. No. 5.1e-16;
Matches 159; Conservative 77; Mismatches 231; Indels 206; Gaps 25;

QY 7 LLLPLLL-----LALPGVGQCPSCGCS-QPQTVFCTARQTTVPDRVPPD 53
Db 17 ILLPFVYLTAQWILCAATAAASAGPQPCVSCSNQFSKVCTRRGLSEVPQIPSN 76

QY 54 TVGLYVFENGITMLDASSFAGLPGQLDLSONQIASLR-----LPRLLLDLSHNSLL 107
Db 77 TRYLMENNIQMIQADTFRHLHLEVLQGRNSIRQIEVGAFNGLASLTLELFDNWL 136

QY 108 ALEPGILDAN-----VEALRLAGLG-----LQOLDEGLFSRLR 141
Db 137 VIPSGAFEYLSKRLRELWLNPNPIESPSYAFNRVPSLMRLDGLKLEYISEGAFEGLF 196

QY 142 N-----LHDLVSDNQLERV-PPVIRGLRGLTRLRAGNTRIA 178
Db 197 NLKYLNGMCNIKDMPNLTPLVGLLELEMSGNHFEIRPGSPHGLSSKLLWM-NSQVS 255

QY 179 QLRPEDLAGLAALQELDVNSLSQALPGDLGLFPRLRLAAA-----RNPFCVCPLSWFG 235
Db 256 LIERNAFQGLASLVELNLAHNLSLPHD---LFTPLRYLVELHLHHPNWCDCDILMLA 312

QY 236 PVRRESHVTLASPEETRCHFPKPNAGRLLELDYADFGCPATTATVTPTRPVVREPTA 295
Db 313 WMLRE-YIPTNSTCCGRCHAPMHMRGRYLVEDVDQASFOCSA-----PFIMDAPRDLNI 364

QY 296 LSSSLAP-----TWLSPTAPA-TEAPSPSTAPPTVGPVPQP-----QDCPPSTC 339
Db 365 SEGRMAELKCRTPPMSSVKWLLPNGTVLSHARHPRISVLNDGTNLFHSLVSDTGVTTC 424

QY 340 -----LNGGTCHLGRHHLACLCPGFTGLYCSEOMGQGTTPSPPTVTP-- 383
Db 425 MGTNVAAGNSAYLNGSTAEINTSNY-----SFFTGTGTETTEISPEDTTRKY 473

QY 384 RPRSLTIGIEPVSTLSRVGLQRYLQGSVQLRSLTYRLNLSGDKELVTLRLPASLA 443
Db 474 KVPVTTSTGYQPAYTTTTLVLIQ-----TRVPKQVA 505

QY 444 EVTVQLRPNATYSVCVMPLGCRVPEGEACGEAHTPPAVHSHNAPVTOAREGNLPLLI 503
Db 506 -----VPATD-----TTDKMQTSLDENVKTK-----II 529

QY 504 APALAVALAALAAAGAAVCVRR---GRAMAAADQKQGVGPGAGLEGEVGVKVPLEPGP 560
Db 530 ICGFVAVTLAAAMLVFFYKLAKRKHQORSTVTAAR-----TVEIIQVD-EDIP 576

QY 561 KATEGGGEALPSG 573
Db 577 AATSAATAAPSG 589

RESULT 14
US-09-520-781-12
; Sequence 12, Application US/09520781
; Patent No. 6689866

; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
; FILE REFERENCE: 15966-540 No. 6689866el Polynucleotides
; CURRENT APPLICATION NUMBER: US/09/520,781
; CURRENT FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: USSN 60/123,667
; PRIOR FILING DATE: 1999-03-09
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 590
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-520-781-12

Query Match 10.6%; Score 333; DB 2; Length 590;
Best Local Similarity 25.8%; Pred. No. 8.7e-16;
Matches 130; Conservative 60; Mismatches 187; Indels 126; Gaps 18;

QY 7 LLLPLLLL-----LALPGVGQCPSCGCS-QPQTVFCTARQTTVPDRVPPD 53
Db 17 ILLPFVYLTAQWILCAATAAASAGPQPCVSCSNQFSKVCTRRGLSEVPQIPSN 76

QY 54 TVGLYVFENGITMLDASSFAGLPGQLDLSONQIASLR-----LPRLLLDLSHNSLL 107
Db 77 TRYLMENNIQMIQADTFRHLHLEVLQGRNSIRQIEVGAFNGLASLTLELFDNWL 136

QY 108 ALEPGILDAN-----VEALRLAGLG-----LQOLDEGLFSRLR 141
Db 137 VIPSGAFEYLSKRLRELWLNPNPIESPSYAFNRVPSLMRLDGLKLEYISEGAFEGLF 196

QY 142 N-----LHDLVSDNQLERV-PPVIRGLRGLTRLRAGNTRIA 178
Db 197 NLKYLNGMCNIKDMPNLTPLVGLLELEMSGNHFEIRPGSPHGLSSKLLWM-NSQVS 255

QY 179 QLRPEDLAGLAALQELDVNSLSQALPGDLGLFPRLRLAAA-----RNPFCVCPLSWFG 235
Db 256 LIERNAFQGLASLVELNLAHNLSLPHD---LFTPLRYLVELHLHHPNWCDCDILMLA 312

QY 236 PVRRESHVTLASPEETRCHFPKPNAGRLLELDYADFGCPATTATVTPTRPVVREPTA 295
Db 313 WMLRE-YIPTNSTCCGRCHAPMHMRGRYLVEDVDQASFOCSA-----PFIMDAPRDLNI 364

QY 296 LSSSLAP-----TWLSPTAPA-TEAPSPSTAPPTVGPVPQP-----QDCPPSTC 339
Db 365 SEGRMAELKCRTPPMSSVKWLLPNGTVLSHARHPRISVLNDGTNLFHSLVSDTGVTTC 424

QY 340 -----LNGGTCHLGRHHLACLCPGFTGLYCSEOMGQGTTPSPPTVTP-- 383
Db 425 MGTNVAAGNSAYLNGSTAEINTSNY-----SFFTGTGTETTEISPEDTTRKY 473

QY 384 RPRSLTIGIEPVSTLSRVGLQ 406
Db 474 KVPVTTSTGYQPAYTTTTLVLIQ 496

RESULT 15
US-09-957-187-12
; Sequence 12, Application US/09957187
; Patent No. 6863889
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.
; APPLICANT: LaRoche, William
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
; FILE REFERENCE: 15966-540 CIP
; CURRENT APPLICATION NUMBER: US/09/957,187
; CURRENT FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/234,082

